

From: Bowman, Amy
Sent: Friday, December 02, 2005 9:43 AM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: FW: sequence search-10/773,678

Hello, this is the search that I requested earlier today. It has been approved for a rush.
Thanks so much for your help,
Amy Bowman

-----Original Message-----

From: Richter, Johann
Sent: Friday, December 02, 2005 9:39 AM
To: Bowman, Amy
Cc: STIC-Biotech/ChemLib
Subject: RE: sequence search-10/773,678

Approved.

Johann R. Richter, Ph.D., Esq.
Supervisory Patent Examiner
Biotechnology and Organic Chemistry
Art Unit 1621
571-272-0646

-----Original Message-----

From: Bowman, Amy
Sent: Friday, December 02, 2005 9:08 AM
To: Richter, Johann
Cc: Bowman, Amy
Subject: FW: sequence search-10/773,678

-----Original Message-----

From: Bowman, Amy
Sent: Friday, December 02, 2005 9:07 AM
To: Chan, Christina; Hutzell, Paula
Subject: FW: sequence search-10/773,678

Hello,
My SPE, Drew Wang, thought I should ask for a rush search for this case. Am I contacting the appropriate person to request this?
Thank you,
Amy Bowman

Point of Contact
P. Sheppard

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

RECEIVED
DEC - 2 2005
STIC/BIOTECH. DIV. (STIC)

12/05/05
JH

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-----Original Message-----
From: Bowman, Amy
Sent: Friday, December 02, 2005 8:54 AM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: FW: sequence search-10/773,678

I meant to mention that this case is about to be allowed, so I will need to include the interference database...

-----Original Message-----
From: Bowman, Amy
Sent: Friday, December 02, 2005 7:31 AM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/773,678

Hello,
I need a search of SEQ ID NO: 342 in application 10/773,678, length limited to 30 nucleobases.
Thank you,
Amy Bowman
AU 1635
REM 2C31
mail REM 2C18
571-272-0755

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:02:55 ; Search time 2155 seconds
(without alignments)
527.549 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactcttcgaggaagcggt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1641224

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb ba:*

2: gb in:*

3: gb env:*

4: gb on:*

5: gb ov:*

6: gb pat:*

7: gb ph:*

8: gb pr:*

9: gb ro:*

10: gb sts:*

11: gb sy:*

12: gb un:*

13: gb vl:*

14: gb htg:*

15: gb pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	80.0	20	6	CQ979199 Sequence
2	14	70.0	20	6	AR120998 Sequence
3	14	70.0	20	6	BD272619 Antisense
4	14	70.0	20	6	AR531367 Sequence
5	13.8	69.0	25	6	AX043113 Sequence
6	13.8	69.0	28	6	AR205609 Sequence
7	13.4	67.0	24	6	AX446884 Sequence
8	13	65.0	19	4	DOGPA45501
9	13	65.0	26	6	AX554614 Sequence
10	13	65.0	26	6	AX703339 Sequence
11	12.8	64.0	20	6	BD228539 IL-17 hom
12	12.8	64.0	20	6	AR359764 Sequence
13	12.8	64.0	27	6	A98434 Sequence 18
14	12.8	64.0	30	6	AX576339 Sequence
15	12.6	63.0	20	6	C0798932 Sequence
16	12.6	63.0	21	6	CQ893797 Sequence
17	12.6	63.0	21	6	AR361504 Sequence
18	12.6	63.0	23	6	AR081003 Sequence

19	12.6	63.0	23	6	I60352
c 20	12.6	63.0	24	6	AX292865
21	12.6	63.0	25	6	CQ628266 Sequence
22	12.6	63.0	25	6	CQ628267 Sequence
23	12.6	63.0	25	6	CQ628268 Sequence
24	12.6	63.0	25	6	CQ628269 Sequence
25	12.6	63.0	25	6	CQ628270 Sequence
26	12.6	63.0	25	6	CQ628271 Sequence
27	12.6	63.0	25	6	CQ628272 Sequence
28	12.6	63.0	25	6	AR469329 Sequence
29	12.6	63.0	25	6	AR469330 Sequence
30	12.6	63.0	25	6	AR469331 Sequence
31	12.6	63.0	25	6	AR469332 Sequence
32	12.6	63.0	25	6	AR469333 Sequence
33	12.6	63.0	25	6	AR469334 Sequence
34	12.6	63.0	25	6	AR469335 Sequence
35	12.6	63.0	26	6	BD133366 Amino aci
36	12.6	63.0	30	6	AR172849 Sequence
37	12.6	63.0	30	6	AX081299 Sequence
38	12.4	62.0	17	6	A89364 Sequence 15
39	12.4	62.0	17	6	BD066877 An antise
40	12.4	62.0	17	6	AX672730 Sequence
41	12.4	62.0	17	6	AX762313 Sequence
42	12.4	62.0	18	6	AX117443 Sequence
c 43	12.4	62.0	20	6	AR098941 Sequence
c 44	12.4	62.0	20	6	AR164768 Sequence
c 45	12.4	62.0	20	6	BD222879 KVLQT1-QT

ALIGNMENTS

RESULT 1	CQ979199	Sequence 201 from Patent WO2004111273.	20 bp	DNA	linear	PAT 19-JAN-2005
LOCUS	CQ979199					
DEFINITION	CQ979199					
ACCESSION	CQ979199.1	GI:57976452				
VERSION						
KEYWORDS						
SOURCE		synthetic construct				
ORGANISM		other sequences; artificial sequences.				
REFERENCE		1				
AUTHORS		Agus, D., Baker, J.B., Natale, R. and Shak, S.				
TITLE		Gene expression markers for response to egfr inhibitor drugs				
JOURNAL		Patent: WO 2004111273-A 201 23-DEC-2004;				
FEATURES		Genomic Health, Inc. (US)				
source		Location/Qualifiers				
		1..20				
		/organism="synthetic construct"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:32630"				
		/note="reverse primer"				

ORIGIN

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Best Local Similarity	100.0%;	Pred. No. 7e+03;		
Matches	16;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Oy	5	CTTCGAGGAGCGGCT 20		
Db	1	CTTCGAGGAGCGGCT 16		
RESULT 2				
AR120998				
LOCUS	AR120998	Sequence 19 from patent US 6159694.	20 bp	DNA
DEFINITION	AR120998			
ACCESSION	AR120998			
VERSION	AR120998.1	GI:14104574		
KEYWORDS		Unknown.		
SOURCE		Unknown.		
ORGANISM		Unknown.		

Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Karas, J.G.
TITLE Antisense modulation of stat3 expression
JOURNAL Patent: US 6159694-A 19 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 70.0%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAA 14
|||||
Db 7 GACTCTTGCAGGAA 20

RESULT 3
BD272619
LOCUS BD272619 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense oligonucleotide modulation of STAT3 expression.
ACCESSION BD272619
VERSION BD272619.1 GI:33082387
KEYWORDS JP 2002541784-A/19
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 20)
AUTHORS Karas, J.G.
TITLE Antisense oligonucleotide modulation of STAT3 expression
JOURNAL Patent: JP 2002541784-A 19 10-DEC-2002;
JOURNAL ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002541784-A/19
PD 10-DEC-2002
PF 06-APR-2000 JP 2000611544
PR 08-APR-1999 US 09/288461
PI JAMES G KARRAS
PC C12N15/09,A61K31/711,A61K48/00,A61P29/00,A61P35/00,
PC A61P37/02,
PC A61P43/00,C12N5/06,C12Q1/02,C12N15/00,C12N5/00 CC Antisense oligonucleotide
FH Key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source 1..20
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 70.0%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAA 14
|||||
Db 7 GACTCTTGCAGGAA 20

RESULT 4
AR531367
LOCUS AR531367 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 19 from patent US 6727064.
ACCESSION AR531367
VERSION AR531367.1 GI:53919806
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Karas, J.G.
TITLE Antisense oligonucleotide modulation of STAT3 expression
JOURNAL Patent: US 6727064-A 19 27-APR-2004;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 70.0%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAA 14
|||||
Db 7 GACTCTTGCAGGAA 20

RESULT 5
AX043113
LOCUS AX043113 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 679 from Patent WO0065088.
ACCESSION AX043113
VERSION AX043113.1 GI:11341721
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 679 02-NOV-2000;
JOURNAL Amersham Pharmacia Biotech AB (SE)
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DPA1 Heterozygote Primer Sequence"

ORIGIN
Query Match 69.0%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 9e+04; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGCT 20
|||||
Db 9 TTTTGCAGGAAGAGGCT 25
|||||

RESULT 6
AR205609
LOCUS AR205609 28 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 13 from patent US 6369038.
ACCESSION AR205609
VERSION AR205609.1 GI:21503235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)
AUTHORS Blumenfeld, M., Brandys, P., d'Auriol, L. and Vasseur, M.
TITLE Closed antisense and sense oligonucleotides and their applications
JOURNAL Patent: US 6369038-A 13 09-APR-2002;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

```

Query Match      69.0%; Score 13.8; DB 6; Length 28;
Best Local Similarity 88.2%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CTCTTGCGGAGCGGC 19
    ||||| ||||| |||||
DB 12 CTCTTGCGGAGCGGC 28

RESULT 7
AX446884
LOCUS AX446884 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 3339 from Patent WO0216649.
ACCESSION AX446884
VERSION AX446884.1 GI:21695783
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 3339 28-FEB-2002;
Illumina, Inc. (US)
FEATURES
source Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."

ORIGIN
Query Match      67.0%; Score 13.4; DB 6; Length 24;
Best Local Similarity 93.3%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTGCAGGAGCGGCT 20
    ||||| ||||| |||||
DB 6 TGCAGGAGCGGCT 20

RESULT 8
DOGP45501
LOCUS DOGP45501 19 bp DNA linear MAM 22-JAN-1996
DEFINITION Dog (Clone: CXX.455) primer for STS 455, 5' end.
ACCESSION L24340
VERSION L24340.1 GI:402053
KEYWORDS PCR identification; PCR primer; STS.
SEGMENT 1 of 2
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (Bases 1 to 19)
AUTHORS Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
TITLE One hundred and one new simple sequence repeat-based markers for
the canine genome
JOURNAL Mamm. Genome 6 (3), 192-195 (1995)
PUBMED 7749226
COMMENT Original source text: Canis familiaris (library: E. Ostrander, in
pBluescript+) adult spleen DNA.
Submitted by:
Fred Hutchinson Cancer Research Center
Transplantation Biology Dept
1124 Columbia; Mailstop M318
Seattle, WA 98104, USA
e-mail: EOostrander@lbi.gov
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing: 55 or 59 degrees C for 0.45 minutes
Polymerization: 74 degrees C for 1.00 minutes
PCR Cycles: 33

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Final Extension: 74 degrees C for 5.00 minutes.
Location/Qualifiers
1..19
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/tissue_type="spleen"
/dev_stages="adult"
/tissue_lib="E. Ostrander, in pBluescript+"

ORIGIN
primer_bind 1..19
Query Match      65.0%; Score 13; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAAGC 16
    ||||| ||||| |||||
DB 4 TCTTGCAGGAAGC 16

RESULT 9
AX554614
LOCUS AX554614 26 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 168 from Patent WO0246229.
ACCESSION AX554614
VERSION AX554614.1 GI:25898281
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Casman,S.J., Padigaru,M., Burgess,C.E., Shimkets,R.A., Spytek,K.A.,
Gilbert,J.A., Mayotte,J.E., Baumgartner,J.C., Mishra,V.,
Vernet,C.A., Dickinson,K.S., Ballinger,R.A. and Wolenc,A.R.
TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0246229-A 168 13-JUN-2002;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer Sequence"

ORIGIN
Query Match      65.0%; Score 13; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAAGC 16
    ||||| ||||| |||||
DB 3 TCTTGCAGGAAGC 15

RESULT 10
AX703339
LOCUS AX703339 26 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 568 from Patent WO0205913.
ACCESSION AX703339
VERSION AX703339.1 GI:29538385
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Li,L., Ballinger,R.A., Padigaru,M., Kekuda,R., Colman,S.D.,
Spytek,K.A., Casman,S.J., Vernet,C.A., Shenoy,S.G., Gusev,V.,
Malyankar,U.M., Edinger,S., Gerlach,V., Smithson,G., Stone,D.J.,
Sciore,P., Macdougall,J.R., Gunther,E., Peyman,J.A., Ellerman,K.,
Gangolli,E.A. and Willet,I.
TITLE G-protein coupled receptors and nucleic acids encoding same
JOURNAL Patent: WO 0205913-A 568 01-AUG-2002;

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source
1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 2.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGCGGC 19
||| ||| ||| ||| ||| ||| |||
Db 10 TCCTGCAAGAGCGGC 25

RESULT 15
LOCUS CQ798932 20 bp DNA linear PAT 28-APR-2004
DEFINITION Sequence 13 from Patent WO2004031412.
ACCESSION CQ798932
VERSION CQ798932.1 GI:46847945
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nakamura,Y. and Katagiri,T.
TITLE Method for diagnosing pancreatic cancer
JOURNAL Patent: WO 2004031412-A 13 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially synthesized primer sequence for
RT-PCR"

ORIGIN

Query Match 63.0%; Score 12.6; DB 6; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAGCGCT 20
||| ||| ||| ||| ||| ||| |||
Db 20 AATCTCCAGGAGCTGCT 2

RESULT 16
LOCUS CQ893797 21 bp DNA linear PAT 01-NOV-2004
DEFINITION Sequence 85 from Patent WO2004087903.
ACCESSION CQ893797
VERSION CQ893797.1 GI:55166196
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Liu,W., Wu,L., Channavaiahala,P.L., Lin,L.L. and Zhang,Y.
TITLE Novel proteins homologous to kinase suppressor of ras
JOURNAL Patent: WO 2004087903-A 85 14-OCT-2004;
Wyeth (US)
FEATURES
source
1. .21
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 63.0%; Score 12.6; DB 6; Length 21;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGCGGC 19
||| ||| ||| ||| ||| ||| |||
Db 3 GACAAATTGCTGGAAGCTGC 21

RESULT 17
LOCUS AR361504 21 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 30 from patent US 6599728.
ACCESSION AR361504
VERSION AR361504.1 GI:33769352
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Morin,G.B., Funk,W.D. and Piatyszek,M.A.
TITLE Second mammalian tankyrase
JOURNAL Patent: US 6599728-A 30 29-JUL-2003;
Geron Corporation; Menlo Park, CA
FEATURES
source
1. .21
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 63.0%; Score 12.6; DB 6; Length 21;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGCGGC 19
||| ||| ||| ||| ||| ||| |||
Db 3 GACAAATTGCTGGAAGCTGC 21

RESULT 18
LOCUS AR081003 23 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 86 from patent US 5969122.
ACCESSION AR081003
VERSION AR081003.1 GI:10007731
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hammond,P.W. and Endozo,A.A.
TITLE Nucleic acid hybridization assay probes, helper probes and
amplification oligonucleotides targeted to mycoplasma pneumoniae
nucleic acid
JOURNAL Patent: US 5969122-A 86 19-OCT-1999;
Location/Qualifiers
source
1. .23
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 63.0%; Score 12.6; DB 6; Length 23;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGCGGC 19
||| ||| ||| ||| ||| ||| |||
Db 5 GACTCTAGCAGGCAATGCGC 23

RESULT 19
160352
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LOCUS I60352 23 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 86 from patent US 5656427.
ACCESSION I60352
VERSION I60352.1 GI:2478797
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hammond, P.W. and Endozo, A.A.
TITLE Nucleic acid hybridization assay probes, helper probes and amplification oligonucleotides targeted to Mycoplasma pneumoniae nucleic acid
JOURNAL Patent: US 5656427-A 86 12-AUG-1997;
FEATURES source
Location/Qualifiers
1..23
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 23;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAGCGGC 19
||||| |||||
Db 5 GACTCTAGCAGCGCATGCG 23
||||| |||||

RESULT 20
AX292865/c
LOCUS AX292865 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 4627 from Patent WO0179548.
ACCESSION AX292865
VERSION AX292865.1 GI:17054548
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 4627 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN
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Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAGCGGCT 20
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Db 23 ACTGCTGCACTAAGCGCT 5
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RESULT 21
CQ628266
LOCUS CQ628266 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13006 from Patent WO0192524.
ACCESSION CQ628266
VERSION CQ628266.1 GI:41678484
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

LOCUS I60352 23 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 86 from patent US 5656427.
ACCESSION I60352
VERSION I60352.1 GI:2478797
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hammond, P.W. and Endozo, A.A.
TITLE Nucleic acid hybridization assay probes, helper probes and amplification oligonucleotides targeted to Mycoplasma pneumoniae nucleic acid
JOURNAL Patent: US 5656427-A 86 12-AUG-1997;
FEATURES source
Location/Qualifiers
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QY 1 GACTCTTGCAGGAGCGGC 20
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Db 7 AGTCTGCCAGAAAGCGCT 25
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RESULT 22
CQ628267
LOCUS CQ628267 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13007 from Patent WO0192524.
ACCESSION CQ628267
VERSION CQ628267.1 GI:41678485
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13007 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES source
Location/Qualifiers
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Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAGCGGCT 20
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Db 6 AGTCTGCCAGAAAGCGCT 24
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RESULT 23
CQ628268
LOCUS CQ628268 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13008 from Patent WO0192524.
ACCESSION CQ628268
VERSION CQ628268.1 GI:41678486
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle

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JOURNAL Patent: WO 0192524-A 13008 06-DEC-2001;
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Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 ACTCTTGCGAGGAGCGGCT 20
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Db 3 AGTCTGCGCAGAGCGGCT 21
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RESULT 26
LOCUS CQ628271 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13011 from Patent WO0192524.
ACCESSION CQ628271
VERSION CQ628271.1 GI:41678489
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13011 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 ACTCTTGCGAGGAGCGGCT 20
||| ||| ||| ||| ||| |||
Db 2 AGTCTGCGCAGAGCGGCT 20
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RESULT 27
LOCUS CQ628272 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13012 from Patent WO0192524.
ACCESSION CQ628272
VERSION CQ628272.1 GI:41678490
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13012 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES source
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 63.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 ACTCTTGCGAGGAGCGGCT 20
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Db 2 AGTCTGCGCAGAGCGGCT 20
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RESULT 25
LOCUS CQ628270 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13010 from Patent WO0192524.
ACCESSION CQ628270
VERSION CQ628270.1 GI:41678488
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13010 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 ACTCTTGCGAGGAGCGGCT 20
||| ||| ||| ||| ||| |||
Db 4 AGTCTGCGCAGAGCGGCT 22
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RESULT 24
LOCUS CQ628269 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13009 from Patent WO0192524.
ACCESSION CQ628269
VERSION CQ628269.1 GI:41678487
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13009 06-DEC-2001;
Aeomica, Inc. (US)
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Qy 2 ACTCTTGCGAGGAGCGGCT 20
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Db 5 AGTCTGCGCAGAGCGGCT 23
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Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAGCGGCT 20
Db 1 AGTCTGCCAGAGCGGCT 19
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19

RESULT 28
AR469329
LOCUS AR469329 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13006 from patent US 6686188.
ACCESSION AR469329
VERSION AR469329.1 GI:42704386
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13006 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
FEATURES
source Location/Qualifiers
1..25
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/mol_type="genomic DNA"
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Query Match 63.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAGCGGCT 20
Db 7 AGTCTGCCAGAGCGGCT 25
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25

RESULT 29
AR469330
LOCUS AR469330 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13007 from patent US 6686188.
ACCESSION AR469330
VERSION AR469330.1 GI:42704387
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13007 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
FEATURES
source Location/Qualifiers
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/organism="unknown"
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Query Match 63.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAGCGGCT 20
Db 6 AGTCTGCCAGAGCGGCT 24
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24

RESULT 30
AR469331
LOCUS AR469331 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13008 from patent US 6686188.
ACCESSION AR469331
VERSION AR469331.1 GI:42704388
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13008 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
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source Location/Qualifiers
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/mol_type="genomic DNA"
ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAGCGGCT 20
Db 5 AGTCTGCCAGAGCGGCT 23
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23

RESULT 31
AR469332
LOCUS AR469332 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13009 from patent US 6686188.
ACCESSION AR469332
VERSION AR469332.1 GI:42704389
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13009 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
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Qy 2 ACTCTTGAGGAGCGGCT 20
Db 4 AGTCTGCCAGAGCGGCT 22
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22

RESULT 32
AR469333
LOCUS AR469333 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13010 from patent US 6686188.
ACCESSION AR469333
VERSION AR469333.1 GI:42704390

TITLE										Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle									
JOURNAL										Patent: US 6686188-A 13012 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;									
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QY										2 ACTCTTGCAGGAAGCGGCT 20									
Db																			
										1 AGTCCTGCCAGAGCGGCT 19									
RESULT 35										BD133366/c									
LOCUS										BD133366 26 bp DNA linear PAT 18-SEP-2000									
DEFINITION										Amino acid sequence of antigen epitope recognized by anticancer human monoclonal antibody CLN-1gG and DNA nucleotide sequence encoding it.									
ACCESSION										BD133366									
VERSION										BD133366.1 GI:23228311									
KEYWORDS										JP 2002051785-A/9.									
SOURCE										synthetic construct									
ORGANISM										other sequences; artificial sequences.									
REFERENCE										1 (bases 1 to 26)									
AUTHORS										Hagiwara, H. and Aotsuka, Y.									
TITLE										Amino acid sequence of antigen epitope recognized by anticancer human monoclonal antibody CLN-1gG and DNA nucleotide sequence									
JOURNAL										Patent: JP 2002051785-A 9 19-FEB-2002; YOSHITHIDE HAGIWARA, HIDEAKI HAGIWARA									
COMMENT										OS Artificial Sequence									
										PN JP 2002051785-A/9									
										PD 19-FEB-2002									
										PF 09-AUG-2000 JP 2000241927									
										PI HIDEAKI HAGIWARA, YASUYUKI AOTSUKA									
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QY										1 GACTCTTGCAGGAAGCGGC 19									
Db																			
										22 GCCCGCTGCAGGATCGGC 4									
RESULT 36										AR172849									
LOCUS										AR172849 30 bp DNA linear PAT 17-DEC-2000									
DEFINITION										Sequence 8 from patent US 6303365.									
ACCESSION										AR172849									
VERSION										AR172849.1 GI:17912340									
KEYWORDS										Unknown.									
SOURCE																			

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Martin,W.Frank., Hain,R., Tietjen,K.-G., Busch,M. and Kloti,A.S.
TITLE Method of determining activity of 1-deoxy-D-xylulose-5-phosphate reductoisomerase and 1-deoxy-D-xylulose-5-phosphate synthase
JOURNAL Patent: US 6303365-A 8 16-OCT-2001;
FEATURES Location/Qualifiers
source 1..30
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Query Match 63.0%; Score 12.6; DB 6; Length 30;
Best Local Similarity 78.9%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGCGGC 19
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Db 8 GACTCATGCATGAACTGGC 26

RESULT 37
AX081299 30 bp DNA linear PAT 27-FEB-2001
LOCUS Sequence 8 from Patent WO0109341.
DEFINITION AX081299
ACCESSION AX081299
VERSION AX081299.1 GI:13170149
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1
AUTHORS Hain,R., Tietjen,K.G., Busch,M., Martin,W.F. and Kloeti,A.S.
TITLE Method of determining the activity of
1-deoxy-d-xylulose-5-phosphate reductoisomerase and
1-deoxy-d-xylulose-5-phosphate synthase
JOURNAL Patent: WO 0109341-A 8 08-FEB-2001;
Bayer Aktiengesellschaft (DE)
FEATURES Location/Qualifiers
source 1..30
/organism="Arabidopsis thaliana"
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Best Local Similarity 78.9%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGCGGC 19
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Db 8 GACTCATGCATGAACTGGC 26

RESULT 38
A89364 17 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 1512 from Patent WO9833904.
DEFINITION A89364
ACCESSION A89364
VERSION A89364.1 GI:6737934
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified
1 (bases 1 to 17)
Brysch,W. and Schlingensiepen,K.
AUTHORS AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
TITLE Patent: WO 9833904-A 1512 06-AUG-1998;
JOURNAL BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES Location/Qualifiers

source 1..17
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 62.0%; Score 12.4; DB 6; Length 17;
Best Local Similarity 92.9%; Pred. No. 4.7e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ACTCTTGCAGGAG 15
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Db 4 ACTCTTGCAGGTAG 17

RESULT 39
BD066877 17 bp DNA linear PAT 27-AUG-2002
LOCUS An antisense oligonucleotide preparation method.
DEFINITION BD066877
ACCESSION BD066877
VERSION BD066877.1 GI:22612480
KEYWORDS JP 2001511000-A/1512.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1512 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1512
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PI 31-JAN-1997 EP 97101531.8
PC KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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/organism="Unknown".
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ORIGIN
Query Match 62.0%; Score 12.4; DB 6; Length 17;
Best Local Similarity 92.9%; Pred. No. 4.7e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ACTCTTGCAGGAG 15
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Db 4 ACTCTTGCAGGTAG 17

RESULT 40
AX672730 17 bp DNA linear PAT 27-MAR-2003
LOCUS Sequence 1175 from Patent WO03004526.
DEFINITION AX672730
ACCESSION AX672730
VERSION AX672730.1 GI:29331078
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Teleman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as

JOURNAL medicines
Patent: WO 03004526-A 1175 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"

ORIGIN

Query Match 62.0%; Score 12.4; DB 6; Length 17;
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAAGCGGCT 20

Db 3 TCCAGGAAGCGGCT 16

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Job time : 2157 secs

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 11:16:05 ; Search time 476 Seconds
(without alignments)
280.029 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactcttgacggaagcggt 20

Scoring table: IDENTITY_NUC

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Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 4138570

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	19	95.0	20	ADZ11150	Human STA
5	18	90.0	20	ADZ11152	Human STA
6	17	85.0	20	ADZ11149	Human STA
7	17	85.0	20	ADZ11153	Human STA
8	16	80.0	20	ADZ11154	Human STA
9	15	75.0	20	ADZ11154	Human STA
10	15	75.0	20	ADZ11148	Human STA
11	14.4	72.0	29	AAT78506	Thiol-8pe
12	14	70.0	20	AAC93168	Human STA
13	14	70.0	20	AAS96785	Human STA
14	14	70.0	20	ADZ10828	Human STA
15	13.8	69.0	25	AAC96250	HLA DP1
16	13.8	69.0	28	AAC96250	Circular
17	13.6	68.0	20	ADZ14825	Human mPG
18	13.6	68.0	30	ADR45889	PCR prime
19	13.6	68.0	30	ADR45885	PCR prime

20	13.6	68.0	30	13	ADR45887	AdR45887 PCR prime
21	13.4	67.0	24	6	ABQ03332	Oligonucleotide
22	13.2	66.0	23	3	AZ89440	Human typ
23	13.2	66.0	25	12	ADH72962	M. tuberc
24	13	65.0	15	4	AAF46591	IGFBP3 ol
25	13	65.0	15	4	AAF46590	IGFBP3 ol
26	13	65.0	15	4	AAF46589	IGFBP3 ol
27	13	65.0	25	12	ADP14476	Renal cel
28	13	65.0	26	6	ABS59220	Human G-p
29	13	65.0	26	6	ABT04530	Human G-p
30	13	65.0	26	6	ABT05715	GPCR rela
31	13	65.0	26	12	ADH31280	Human G-p
32	12.8	64.0	24	12	ADK98351	Primer of
33	12.8	64.0	25	9	AC112520	Human mic
34	12.8	64.0	25	9	ACH63464	DNA targe
35	12.8	64.0	25	9	ACH51423	DNA targe
36	12.8	64.0	25	9	ACH53400	DNA targe
37	12.8	64.0	27	2	AAX22793	PCR prime
38	12.8	64.0	27	10	ADC51654	5' PCR pr
39	12.8	64.0	30	10	ABZ21923	Mouse fus
40	12.6	63.0	20	12	ADM92376	Pancreat
41	12.6	63.0	20	12	ADM14384	Human mPG
42	12.6	63.0	20	12	ADM14826	Human mPG
43	12.6	63.0	21	11	ADP19693	Periodont
44	12.6	63.0	21	13	ADR67642	Human ret
45	12.6	63.0	21	13	ADS99597	Small int

ALIGNMENTS

RESULT 1

ADZ11151
ID ADZ11151 standard; DNA; 20 BP.

XX ADZ11151;

XX 16-JUN-2005 (first entry)

XX Human STAT3-specific antisense oligonucleotide - SEQ ID 342.

XX antisense oligonucleotide; antisense therapy; inflammation;
XX antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
XX cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
XX brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
XX phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.

OS Homo sapiens.

XX US2005074879-A1. → instant app.

XX 07-APR-2005.

XX 06-FEB-2004; 2004US-00773678.

XX 06-APR-2000; 2000WO-US009054.

XX 11-JAN-2001; 2001US-00758881.

XX 14-NOV-2003; 2003US-00713139.

XX (KARR/) KARRAS J G.

XX Karas JG;

XX WPI; 2005-272408/28.

XX New antisense compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).

XX Claim 13; SEQ ID NO 342; 149pp; English.

XX The invention comprises antisense oligonucleotides that are targeted to

CC nucleic acid molecules encoding human signal transducers and activators
CC of transcription 3 (STAT3). The antisense oligonucleotides of the
CC invention inhibit expression of human STAT3. The antisense
CC oligonucleotides of the invention are useful for treating and preventing
CC inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
CC breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
CC and lymphomas). The present DNA sequence represents a human STAT3-
CC specific antisense oligonucleotide. NOTE: The present sequence has a
CC phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
xx

Sequence 20 BP: 4 A: 5 C: 7 G: 4 T: 0 U: 0 Other:

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAAGCGGT 20
|||
Db 1 GACTCTTCAGGAAGCGGT 20

RESULT 2	
ADZ10967/c	
ID	ADZ10967 standard; DNA; 29 BP.
XX	
XX	
ADZ10967;	
XX	
XX	
DT	16-JUN-2005 (first entry)
XX	
XX	
DE	Human STAT3-specific nucleotide probe - SEQ ID 158.
XX	
XX	
KW	antisense oligonucleotide; antisense therapy; inflammation;
KW	antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
KW	cancer; cystostatic; breast tumor; prostate tumor; head & neck tumor;
KW	brain tumor; multiple myeloma; leukemia; lymphoma; STAT3;
KW	probe; ss.

The invention comprises antisense oligonucleotides that are targeted to nucleic acid molecules encoding human signal transducers and activators of transcription 3 (STAT3). The antisense oligonucleotides of the invention inhibit expression of human STAT3. The antisense oligonucleotides of the invention are useful for treating and preventing inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g. breast, prostate, head and neck, brain, myelomas, melanomas, leukemias, and lymphomas). The present DNA sequence represents a human STAT3-specific probe.

```

Query Match      100.0%;   Score 20;   DB 14;   Length 29;
Best Local Similarity 100.0%;   Pred. NO. 7.5;
Matches 20;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      1   GACTCTTGCAGGAAGCGGCT 20
          |||||
Db      26   GACTCTTGCAGGAAGCGGCT 7
          |||||

```

RESULT 3
ADZ10988
ID ADZ10988 standard; DNA; 20 BP.
XX
XX AC ADZ10988;
XX
XX
XX 16-JUN-2005 (first entry)
XX DT
XX DE Human STAT3-specific antisense oligonucleotide - SEQ ID 179.

Query Match	95.0%;	Score 19;	DB 14;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 23;		

Qy 1 GACTCTTGCAGGAAGCGC 19
|||
db 2 GACTCTTGCAGGAAGCGC 20
|||

```
RESULT 4
ADZ11150
ID ADZ11150-standard; DNA; 20 BP.
XX
AC ADZ11150;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human STAT3-specific antisense oligonucleotide - SEQ ID 341.
XX
DE antisense oligonucleotide; antisense therapy; inflammation;
KW antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
KW cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
KW brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
KW phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.
XX
OS Homo sapiens.
XX
PN US2005074879-A1.
XX
PD 07-APR-2005.
XX
PF 06-FEB-2004; 2004US-00773678.
XX
PR 06-APR-2000; 2000WO-US009054.
XX
PR 11-JAN-2001; 2001US-00758881.
XX
PR 14-NOV-2003; 2003US-00713139.
XX
PA (KARR/) KARRAS J G.
XX
PI Karas JG;
XX
PI WPI; 2005-272408/28.
XX
DR New antisense compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).
XX
PS Example 19; SEQ ID NO 341; 149pp; English.
XX
SS The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 95.0%; Score 19; DB 14; Length 20;
Best Local Similarity 100.0%; Pred.No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ACTCTTGCAGGAGCGCT 20
Db 1 ACTCTTGCAGGAGCGCT 19
RESULT 5
ADZ11152
ID ADZ11152 standard; DNA; 20 BP.
XX
AC ADZ11152;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human STAT3-specific antisense oligonucleotide - SEQ ID 343.
XX
DE antisense oligonucleotide; antisense therapy; inflammation;
KW antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
KW cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
KW brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
KW phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.
XX
OS Homo sapiens.
XX
PN US2005074879-A1.
XX
PD 07-APR-2005.
XX
PF 06-FEB-2004; 2004US-00773678.
XX
PR 06-APR-2000; 2000WO-US009054.
XX
PR 11-JAN-2001; 2001US-00758881.
XX
PR 14-NOV-2003; 2003US-00713139.
XX
PA (KARR/) KARRAS J G.
XX
PI Karas JG;
XX
PI WPI; 2005-272408/28.
XX
DR New antisense compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).
XX
PS Example 19; SEQ ID NO 341; 149pp; English.
XX
SS The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 95.0%; Score 19; DB 14; Length 20;
Best Local Similarity 100.0%; Pred.No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ACTCTTGCAGGAGCGCT 20
Db 1 ACTCTTGCAGGAGCGCT 19
RESULT 6
ADZ11149
ID ADZ11149 standard; DNA; 20 BP.
XX
AC ADZ11149;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human STAT3-specific antisense oligonucleotide - SEQ ID 340.
XX
DE antisense oligonucleotide; antisense therapy; inflammation;
KW antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
KW cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
KW brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
KW phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.
XX
OS Homo sapiens.
XX
PN US2005074879-A1.
XX
PD 07-APR-2005.
XX
PF 06-FEB-2004; 2004US-00773678.
XX
PR 06-APR-2000; 2000WO-US009054.
XX
PR 11-JAN-2001; 2001US-00758881.
XX
PR 14-NOV-2003; 2003US-00713139.
XX
PA (KARR/) KARRAS J G.
XX
PI Karas JG;
XX
PI WPI; 2005-272408/28.
XX
DR New antisense compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).
XX
PS Example 19; SEQ ID NO 343; 149pp; English.
XX
SS The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
XX
SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 90.0%; Score 18; DB 14; Length 20;
Best Local Similarity 100.0%; Pred.No. 69;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GACTCTTGCAGGAGCGG 18
Db 3 GACTCTTGCAGGAGCGG 20
```

```

PD 07-APR-2005.
XX
XX
XX 06-FEB-2004; 2004US-00773678.
XX
XX 06-APR-2000; 2000WO-US009054.
XX 11-JAN-2001; 2001US-00758881.
XX 14-NOV-2003; 2003US-00713139.
XX
XX (KARR/) KARRAS J G.
XX
XX Karas JG;
XX
XX WPI; 2005-272408/28.
XX
XX New antisease compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).
XX
XX Example 19; SEQ ID NO 340; 149pp; English.
XX
XX The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
XX
XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 85.0%; Score 17; DB 14; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 TCTTGCAGGAGCGGCT 20
XX |||||
XX 1 TCTTGCAGGAGCGGCT 17
XX
XX Db
XX
XX RESULT 7
XX ADZ11153
XX ID ADZ11153 standard; DNA; 20 BP.
XX
XX AC ADZ11153;
XX
XX 16-JUN-2005 (first entry)
XX
XX Human STAT3-specific antisense oligonucleotide - SEQ ID 344.
XX
XX antisense oligonucleotide; antisense therapy; inflammation;
XX antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
XX cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
XX brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
XX phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.
XX
XX Homo sapiens.
XX
XX US2005074879-A1.
XX
XX 07-APR-2005.
XX
XX 06-FEB-2004; 2004US-00773678.
XX
XX 06-APR-2000; 2000WO-US009054.
XX 11-JAN-2001; 2001US-00758881.
XX 14-NOV-2003; 2003US-00713139.
XX
XX (KARR/) KARRAS J G.
XX
XX Karas JG;
XX
XX WPI; 2005-272408/28.
XX
XX New antisease compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).
XX
XX Example 19; SEQ ID NO 340; 149pp; English.
XX
XX The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
XX
XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 85.0%; Score 17; DB 14; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 TCTTGCAGGAGCGGCT 20
XX |||||
XX 1 TCTTGCAGGAGCGGCT 17
XX
XX Db
XX
XX RESULT 8
XX ADW26449
XX ID ADW26449 standard; DNA; 20 BP.
XX
XX AC ADW26449;
XX
XX 10-MAR-2005 (first entry)
XX
XX EGFR inhibitor cancer treatment prognostic marker PCR primer, SEQ ID 201.
XX
XX prognosis; selectable marker; cancer; cytostatic; ovary tumor;
XX colon tumor; pancreatic cancer; non-small-cell lung cancer; breast tumor;
XX head & neck tumor; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO2004111273-A2.
XX
XX 23-DEC-2004.
XX
XX 28-MAY-2004; 2004WO-US017215.
XX
XX 30-MAY-2003; 2003US-0474908P.
XX
XX (GENO-) GENOMIC HEALTH INC.
XX
XX Agus D, Baker JB, Natale R, Shak S;
XX WPI; 2005-040123/04.
XX
XX Predicting if a subject responds to epidermal growth factor receptor
XX (EGFR) inhibitor treatment, useful for cancer patients, by determining
XX expression level of prognostic RNA transcripts of genes e.g. FUS, or its
XX expression product.
XX
XX Claim 41; SEQ ID NO 201; 77pp; English.
XX
XX The invention comprises a method for predicting the likelihood that a
XX subject will respond to cancer treatment with an epidermal growth factor
XX receptor (EGFR) inhibitor. The method involves determining the expression

```


CC level of one or more prognostic RNA transcripts or their expression
CC products in a biological sample comprising cancer cells obtained from the
CC patient. The method of the invention is useful for predicting whether a
CC patient is likely to respond well to treatment with an EGFR inhibitor,
CC especially patients having: ovarian cancer, colon cancer, pancreatic
CC cancer, non-small cell lung cancer, breast cancer, and head/neck cancer.
CC The present DNA sequence represents a PCR primer which is specific for a
CC prognostic marker of the invention.

XX SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CTTGCAGGAAGCGGCT 20
Db 1 CTTGCAGGAAGCGGCT 16
|||||

RESULT 9
ADZ11154
ID ADZ11154 standard; DNA; 20 BP.

AC ADZ11154;

XX 16-JUN-2005 (first entry)

XX Human STAT3-specific antisense oligonucleotide - SEQ ID 345.

XX antisense oligonucleotide; antisense therapy; inflammation;
XX antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
XX cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
XX brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
XX phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.

XX Homo sapiens.

XX US2005074879-A1.

XX 07-APR-2005.

XX 06-FEB-2004; 2004US-00773678.

XX 06-APR-2000; 2000WO-US009054.

XX 11-JAN-2001; 2001US-00758881.

XX 14-NOV-2003; 2003US-00713139.

XX (KARR/) KARRAS J G.

XX Karras JG;

XX WPI; 2005-272408/28.

XX New antisense compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).

XX Example 19; SEQ ID NO 345; 149pp; English.

XX The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.

XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAG 15
Db 6 GACTCTTGCAGGAAG 20
|||||

RESULT 10

ADZ11148
ID ADZ11148 standard; DNA; 20 BP.

XX ADZ11148;

XX 16-JUN-2005 (first entry)

XX Human STAT3-specific antisense oligonucleotide - SEQ ID 339.

XX antisense oligonucleotide; antisense therapy; inflammation;
XX antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
XX cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
XX brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
XX phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.

XX Homo sapiens.

XX US2005074879-A1.

XX 07-APR-2005.

XX 06-FEB-2004; 2004US-00773678.

XX 06-APR-2000; 2000WO-US009054.

XX 11-JAN-2001; 2001US-00758881.

XX 14-NOV-2003; 2003US-00713139.

XX (KARR/) KARRAS J G.

XX Karras JG;

XX WPI; 2005-272408/28.

XX New antisense compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).

XX Example 19; SEQ ID NO 339; 149pp; English.

XX The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.

XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TTGCAGGAAGCGGCT 20
Db 1 TTGCAGGAAGCGGCT 15
|||||

```

RESULT 11
AAT78506
ID AAT78506 standard; DNA; 29 BP.
XX
AC AAT78506;
XX
DT 10-MAR-1998 (first entry)
XX
DE Thiol-specific antioxidant gene sense primer EukTSA sen.
XX
KW Thiol-specific antioxidant; helminth; cestode; nematode; trematode;
KW anthelmintic; heartworm; infection; therapy; PCR; primer; ss.
XX
OS Synthetic.
OS Dirofilaria immitis.
XX
FN WO9729766-A1.
XX
PD 21-AUG-1997.
XX
PF 13-FEB-1997; 97WO-US002361.
XX
PR 15-FEB-1996; 96US-00602262.
XX
PA (HESK-) HESKA CORP.
XX
PI Klimowski L, Tripp CA;
XX
XX WPI; 1997-424754/39.
XX
XX Nucleic acid encoding thiol-specific antioxidant protein of helminth
PT larvae - useful for treatment or prevention of helminth infection,
PT specifically heartworm.
XX
PS Example 8; Page 68; 88pp; English.
XX
CC This oligonucleotide comprises sense PCR primer EukTSA sen that contains
CC a BamHI site. It was used with antisense primer EukTSA ant (see AAT78507)
CC to amplify the coding region of the Dirofilaria immitis thiol-specific
CC antioxidant (TSA) protein gene (see AAT78497). The 620-nucleotide PCR
CC product was subcloned into the pKB3poly shuttle vector, and a recombinant
CC racoon provirus capable of directing production of TSA in eukaryotic
CC host cells was produced. TSA (see AAW23715) can be used in the treatment
CC or prevention of heartworm
XX
SQ Sequence 29 BP; 6 A; 9 C; 8 G; 6 T; 0 U; 0 Other;
Query Match 72.0%; Score 14.4; DB 2; Length 29;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACTCTTGCGAGGAGC 16
DB 14 GACTCTTGCTGGAAGC 29
|||||
|||||

RESULT 12
AAC93168
ID AAC93168 standard; DNA; 20 BP.
XX
AC AAC93168;
XX
XX
DT 15-FEB-2001 (first entry)
XX
DE Human STAT3 phosphorothioate antisense oligonucleotide SEQ ID NO:19.
XX
KW Human; mouse; STAT3; phosphorothioate; antisense oligonucleotide;
KW modulation; signal transducer and activator of transcription;
KW DNA-binding protein; signal transduction; inhibition; apoptosis;
KW inflammatory disease; cancer; antinflammatory; antirheumatic;
KW cytosolic; immunostimulatory; rheumatoid arthritis; leukaemia; myeloma;
KW melanoma; lymphoma; diagnosis; ss.
XX

OS Homo sapiens.
XX
PN WO2000061602-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009054.
XX
PR 08-APR-1999; 99US-00288461.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Karras JG;
XX
XX WPI; 2000-619223/59.
XX
XX New antisense compound for inhibiting the expression of signal transducer
PT and activator of transcription 3 (STAT3) in cells or tissues and treating
PT diseases or condition associated with STAT3, such as rheumatoid arthritis
PT and cancer.
XX
PS Example 2; Page 46; 104pp; English.
XX
CC The present invention describes an antisense compound (I), 8 to 30
CC nucleobases in length, that is targeted to a nucleic acid molecule
CC encoding STAT3 (Signal Transducer and Activator of Transcription) and
CC which inhibits the expression of it. (I) has antinflammatory,
CC antirheumatic, cytostatic and immunostimulatory activities. (I) is used
CC for inhibiting the expression of STAT3 in cells or tissues, treating an
CC animal having a disease or condition associated with STAT3 or a human
CC having a disease or condition characterised by a reduction in apoptosis,
CC and inducing apoptosis in a cell. Diseases or conditions that are treated
CC are rheumatoid arthritis, cancer of the breast, prostate, brain, head
CC and/or neck, leukaemia, myeloma, melanoma or lymphoma. (I) can also be
CC used for diagnostic methods in detecting and determining the role of
CC STAT3 in various cell functions, physiological processes and conditions
CC for diagnosing the conditions associated with expression of STAT3.
CC (I) can be used alone or with other drugs as an immunostimulator. (I) is
CC used in sandwich and colourimetric assays, involving enzyme conjugation
CC and radiolabeling and is used in diagnostic kits. AAC93150 encodes human
CC STAT3 and AAC93231 encodes mouse STAT3 as given in the exemplification of
CC the present invention. AAC93151 to AAC93230 and AAC93232 to AAC93299
CC represent STAT3 phosphorothioate antisense oligonucleotides, and AAC93300
CC represents a mismatch control oligonucleotide which are used in example
CC from the present invention
XX
SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 70.0%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTCTTGCGAGGAA 14
DB 7 GACTCTTGCGAGGAA 20
|||||
|||||

RESULT 13
AAS96785
ID AAS96785 standard; DNA; 20 BP.
XX
AC AAS96785;
XX
XX
DT 26-FEB-2002 (first entry)
XX
DE Human STAT3 antisense phosphorothioate oligodeoxynucleotide #18.
XX
KW STAT3; human; signal transducer and activator of transcription; ss; STAT;
KW antisense gene therapy; Fas-mediated apoptosis; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; cancer; breast; prostate; head;
KW neck; brain; leukaemia; myeloma; melanoma; lymphoma; apoptosis; ss;
KW antinflammatory; immunosuppressive; antirheumatic; antiarthritic;
KW cytostatic.
XX

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```
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2001029250-A1.
XX PD 11-OCT-2001.
XX PF 11-JAN-2001; 2001US-00758881.
XX PR 08-APR-1999; 99US-00288461.
XX PR 06-APR-2000; 2000WO-US009054.
XX PA (KARR/) KARRAS J G.
XX PI Karras JG;
XX PI WPI; 2002-009991/01.
XX PT Novel antisense compound useful for treating and diagnosing inflammatory
XX PT diseases and cancers, is targeted to a nucleic acid molecule encoding
XX PT signal transducer and activator of transcription proteins.
XX PS Example 2; Page 13; 21pp; English.
XX CC The invention relates to antisense compounds targeted to a nucleic acid
XX CC molecule encoding a signal transducer and activator of transcription
XX CC (STAT) protein, specifically STAT3, where the antisense compounds inhibit
XX CC the expression of STAT3. The antisense sequences are useful for
XX CC inhibiting the expression of STAT3 in cells or tissues, inducing Fas-
XX CC mediated apoptosis in cells, and sensitising cells to apoptosis. They are
XX CC also useful for treating an animal having a disease or condition
XX CC associated with STAT3. These disorders include inflammatory or autoimmune
XX CC disease, particularly rheumatoid arthritis, cancers, such as those of the
XX CC breast, prostate, brain and head and neck and leukemias, myelomas,
XX CC melanomas and lymphomas. Also treatable are human diseases or conditions
XX CC characterised by a reduction in apoptosis or an insensitivity to
XX CC apoptotic signals. The sequences of the invention can be used in clinical
XX CC research, for detecting and determining the role of STAT3 in various cell
XX CC functions and physiological processes and for diagnosing conditions
XX CC associated with the expression of STAT3. The sequences represent cDNA
XX CC encoding human STAT3 and human STAT3 oligonucleotides
XX SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTCGAGAA 14
Db 7 GACTCTTCGAGAA 20

RESULT 14
ADZ10828
ID ADZ10828 standard; DNA; 20 BP.
XX AC ADZ10828;
XX DT 16-JUN-2005 (first entry)
XX DE Human STAT3-specific antisense oligonucleotide - SEQ ID 19.
XX KW antisense oligonucleotide; antisense therapy; inflammation;
XX KW antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
XX KW cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
XX KW brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
XX KW phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.
XX OS Homo sapiens.
XX PN US2005074879-A1.

XX 07-APR-2005.
XX 06-FEB-2004; 2004US-00773678.
XX 06-APR-2000; 2000WO-US009054.
XX 11-JAN-2001; 2001US-00758881.
XX 14-NOV-2003; 2003US-00713139.
XX PA (KARR/) KARRAS J G.
XX PI Karras JG;
XX PI WPI; 2005-272408/28.
XX PT New antisense compound, useful for treating or preventing inflammatory
XX PT diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX PT and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX PT lymphomas).
XX PS Example 2; SEQ ID NO 19; 149pp; English.
XX CC The invention comprises antisense oligonucleotides that are targeted to
XX CC nucleic acid molecules encoding human signal transducers and activators
XX CC of transcription 3 (STAT3). The antisense oligonucleotides of the
XX CC invention inhibit expression of human STAT3. The antisense
XX CC oligonucleotides of the invention are useful for treating and preventing
XX CC inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX CC breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX CC and lymphomas). The present DNA sequence represents a human STAT3-
XX CC specific antisense oligonucleotide. NOTE: The present sequence has a
XX CC phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
XX SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTCGAGAA 14
Db 7 GACTCTTCGAGAA 20

RESULT 15
AAC96250
ID AAC96250 standard; DNA; 25 BP.
XX AC AAC96250;
XX DT 26-FEB-2001 (first entry)
XX DE HLA DPA1 gene PCR primer #7.
XX KW DNA sequence analysis; sequencing; protein sequence; protein structure;
XX KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
XX KW human leukocyte antigen; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO2000065088-A2.
XX PD 02-NOV-2000.
XX PF 20-APR-2000; 2000WO-EP003636.
XX PR 26-APR-1999; 99EP-00303215.
XX PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX PI Ulfendahl P, Wong K;
XX PI WPI; 2000-679677/66.
```

XX Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
XX Claim 14; Page 48; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
XX Sequence 25 BP; 4 A; 2 C; 6 G; 13 T; 0 U; 0 Other;
SQ
Query Match 69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGCT 20
Db 9 TTTTGCAGGAAGCGGCT 25

RESULT 16
AAQ31029
ID AAQ31029 standard; RNA; 28 BP.
XX
XX AC AAQ31029;
XX
XX 25-MAR-2003 (revised)
DT 23-MAR-1993 (first entry)
XX
XX Circular antisense oligonucleotide GT to inhibit HSV-1.
XX
XX Closed oligonucleotide; immunomodulation; antiviral; antitumour;
KW exonuclease resistant; Herpes Simplex virus; cyclic; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1
FT /*tag= a
FT /note= "forms phosphodiester bond with 3'-OH of C at
FT position 28"
FT 28
FT misc_feature b
FT /*tag= b
FT /note= "forms phosphodiester bond with 5'-Phosphate group
FT of G at position 1"
XX
XX WO9219732-A1.
PN
XX
XX 12-NOV-1992.
PD
XX
XX 24-APR-1992; 92WO-FR000370.
PF
XX
XX 25-APR-1991; 91FR-00005114.
PR
XX
XX (GEST) GENSET.
PA
XX
XX Blumenfeld M, Brandys P, Dauriol L, Vasseur M;
XX WPI; 1992-398859/48.
XX
XX Cyclic sense or anti-sense closed oligo nucleotide(s) - useful for
XX therapeutic antiviral or anticancer agent, labelled diagnostic or
PT cosmetic applications, and natural immunomodulatory interferon inducer.
XX
XX Example 6; Page 50; 85pp; French.
XX

CC This is an example of a cyclic oligonucleotide of the invention. The
CC closed oligonucleotides are more resistant to exonuclease attack than
CC their linear counterparts. The nucleotides at position 1 and 28 are
CC brought into proximity for ligation by hybridisation to a complementary
CC linear oligonucleotide. The circularised form of oligonucleotide GT
CC inhibits HSV-1 multiplication (30% inhibition at 2microm and 65%
CC inhibition at 5microm). At these low concentrations, the circular
CC oligonucleotide has a higher inhibitory effect than its linear
CC counterpart. See AAQ31019-Q31028 for other examples. (Updated on 25-MAR-
CC 2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 28 BP; 3 A; 8 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 2; Length 28;
Best Local Similarity 88.2%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CTCTTGCAGGAAGCGGC 19
Db 12 CTCTTGCAGGAAGCGGC 28

RESULT 17
ADM14825/c
ID ADM14825 standard; DNA; 20 BP.
XX
XX AC ADM14825;
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1012.
DE
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX Key Location/Qualifiers
XX modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
PN
XX
XX 08-APR-2004.
PD
XX
XX 25-SEP-2003; 2003WO-US030374.
PF
XX
XX 25-SEP-2002; 2002US-0413549P.
PR
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
PI
XX
XX WPI; 2004-305094/28.
DR

XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 1012; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 12; Length 20;
Best Local Similarity 80.0%; Pred. No. 9.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACTCTTCAGGAGCGGCT 20
||| ||||| ||||| |||||
Db 20 GATTCCTGCAGCAAGTGCT 1

RESULT 18
ADR45889
ID ADR45889 standard; DNA; 30 BP.
XX
AC ADR45889;
XX
DT 18-NOV-2004 (first entry)
XX
DE PCR primer used to amplify the VPS28 mutant Vps28deltaN.
XX
KW viral budding; viral infectivity; enveloped virus; VPS28 protein;
KW TSG101 protein; human immunodeficiency virus; HIV-1; HIV-II;
KW Marburg virus; Ebola virus; small interfering RNA; siRNA;
KW viral infection; HIV infection; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO2004071462-A2.
XX
PD 26-AUG-2004.
XX
PF 12-FEB-2004; 2004WO-US004518.
XX
PR 12-FEB-2003; 2003US-0446909P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
PA (FUNC-) FUNCTIONAL GENETICS INC.
XX
PI Yu X, Liu B, Li L;
XX WPI; 2004-615918/59.
DR
PT Reducing viral budding and infectivity from a human cell infected by an
PT enveloped virus (e.g. HIV) comprises contacting the cell with an agent
PT that modulates the interaction between a VPS28 protein and a TSG101

PT protein.
XX
XX Example; SEQ ID NO 10; 71pp; English.
XX
CC The specification describes a method for reducing viral budding and
CC infectivity from a mammalian cell infected by an enveloped virus. The
CC method comprises contacting the mammalian cell with an agent that
CC modulates the interaction between a VPS28 protein and a TSG101 protein or
CC that regulates the expression of a VPS28 gene, or an antibody that binds
CC a VPS28 protein. The enveloped virus is selected from human
CC immunodeficiency virus (HIV) type-I, HIV-II, Marburg virus and Ebola
CC virus. The agent especially comprises a small interfering RNA (siRNA)
CC targeting the VPS28 gene. The method of the invention is useful for
CC treating viral infections, including HIV infections. It may also be used
CC for evaluating and screening drugs that can be used for treating viral
CC infections. PCR primers ADR45888-ADR45889 were used to amplify a VPS28
CC mutant. The amplified product was used to produce vectors for use in the
CC method of the invention.

SQ Sequence 30 BP; 8 A; 5 C; 11 G; 6 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 13; Length 30;
Best Local Similarity 80.0%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACTCTTCAGGAGCGGCT 20
||| ||||| ||||| |||||
Db 8 GAGGCATGCAGCAAGCGGTT 27

RESULT 19
ADR45885
ID ADR45885 standard; DNA; 30 BP.

XX ADR45885;

AC ADR45885;

DT 18-NOV-2004 (first entry)

DE PCR primer used to amplify a human VPS28-Flag fusion.
XX
KW viral budding; viral infectivity; enveloped virus; VPS28 protein;
KW TSG101 protein; human immunodeficiency virus; HIV-1; HIV-II;
KW Marburg virus; Ebola virus; small interfering RNA; siRNA;
KW viral infection; HIV infection; PCR; primer; ss.

OS Synthetic.

PN WO2004071462-A2.

XX 26-AUG-2004.

XX 12-FEB-2004; 2004WO-US004518.

XX 12-FEB-2003; 2003US-0446909P.

XX (UYJO) UNIV JOHNS HOPKINS.
XX (FUNC-) FUNCTIONAL GENETICS INC.

XX Yu X, Liu B, Li L;

XX WPI; 2004-615918/59.

DR Reducing viral budding and infectivity from a human cell infected by an
DR enveloped virus (e.g. HIV) comprises contacting the cell with an agent
DR that modulates the interaction between a VPS28 protein and a TSG101
DR protein.

XX Example; SEQ ID NO 6; 71pp; English.

XX The specification describes a method for reducing viral budding and
XX infectivity from a mammalian cell infected by an enveloped virus. The
XX method comprises contacting the mammalian cell with an agent that
XX modulates the interaction between a VPS28 protein and a TSG101 protein or

CC that regulates the expression of a VPS28 gene, or an antibody that binds
CC a VPS28 protein. The enveloped virus is selected from human
CC immunodeficiency virus (HIV) type-I, HIV-II, Marburg virus and Ebola
CC virus. The agent especially comprises a small interfering RNA (siRNA)
CC targeting the VPS28 gene. The method of the invention is useful for
CC treating viral infections, including HIV infections. It may also be used
CC for evaluating and screening drugs that can be used for treating viral
CC infections. PCR primers ADR45884-ADR45885 were used to amplify a VPS28-
CC Flag fusion construct. The amplified product was used to produce vectors
CC for use in the method of the invention.

XX
XX
SQ Sequence 30 BP; 8 A; 5 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 13; Length 30;
Best Local Similarity 80.0%; Pred. No. 1e+04; 4; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GACTCTTTCAGGAGCGGCT 20
||| |||||
Db 8 GAGGCATGCAGGAGCGGTT 27

RESULT 20

ADR45887
ID ADR45887 standard; DNA; 30 BP.

XX
XX AC ADR45887;

XX
XX DT 18-NOV-2004 (first entry)

XX
XX DE PCR primer used to amplify the VPS28 mutant Vps28deltaN1.

XX
XX KW viral budding; viral infectivity; enveloped virus; VPS28 protein;

XX
XX TSGL101 protein; human immunodeficiency virus; HIV-1; HIV-II;

XX
XX KW Marburg virus; Ebola virus; small interfering RNA; siRNA;

XX
XX KW viral infection; HIV infection; PCR; primer; ss.

XX
XX OS Synthetic.

XX
XX PN WO2004071462-A2.

XX
XX PD 26-AUG-2004.

XX
XX PF 12-FEB-2004; 2004WO-US004518.

XX
XX PR 12-FEB-2003; 2003US-0446909P.

XX
XX PA (UYJO) UNIV JOHNS HOPKINS.

XX
XX PA (FUNC-) FUNCTIONAL GENETICS INC.

XX
XX PI Yu X, Liu B, Li L;

XX
XX DR WPI; 2004-615918/59.

XX
XX PT Reducing viral budding and infectivity from a human cell infected by an
XX enveloped virus (e.g. HIV) comprises contacting the cell with an agent
XX that modulates the interaction between a VPS28 protein and a TSGL101
XX protein.

XX
XX PS Example; SEQ ID NO 8; 71pp; English.

XX
XX CC The specification describes a method for reducing viral budding and
XX infectivity from a mammalian cell infected by an enveloped virus. The
XX method comprises contacting the mammalian cell with an agent that
XX modulates the interaction between a VPS28 protein and a TSGL101 protein or
XX that regulates the expression of a VPS28 gene, or an antibody that binds
XX a VPS28 protein. The enveloped virus is selected from human
XX immunodeficiency virus (HIV) type-I, HIV-II, Marburg virus and Ebola
XX virus. The agent especially comprises a small interfering RNA (siRNA)
XX targeting the VPS28 gene. The method of the invention is useful for
XX treating viral infections, including HIV infections. It may also be used
XX for evaluating and screening drugs that can be used for treating viral
XX infections. PCR primers ADR45886-ADR45887 were used to amplify a VPS28

CC mutant. The amplified product was used to produce vectors for use in the
CC method of the invention.

XX
XX SQ Sequence 30 BP; 8 A; 5 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 13; Length 30;
Best Local Similarity 80.0%; Pred. No. 1e+04; 4; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GACTCTTTCAGGAGCGGCT 20
||| |||||
Db 8 GAGGCATGCAGGAGCGGTT 27

RESULT 21

ABQ03332
ID ABQ03332 standard; DNA; 24 BP.

XX
XX AC ABQ03332;

XX
XX DT 11-JUN-2002 (first entry)

XX
XX DE Oligonucleotide adapter/capture probe 3323.

XX
XX KW Oligonucleotide array; adapter sequence; probe; ss.

XX
XX OS Synthetic.

XX
XX PN WO200216649-A2.

XX
XX PD 28-FEB-2002.

XX
XX PF 27-AUG-2001; 2001WO-US026519.

XX
XX PR 25-AUG-2000; 2000US-0227948P.

XX
XX PR 29-AUG-2000; 2000US-0228854P.

XX
XX PA (ILLU-) ILLUMINA INC.

XX
XX PI Gunderson K;

XX
XX DR WPI; 2002-292068/33.

XX
XX PT Array comprising adapter sequences useful for immobilizing or detecting a
XX target nucleic acid sequence, has different addresses comprising
XX different specific capture probes.

XX
XX PS Claim 1; Page 123; 261pp; English.

XX
XX CC The invention relates to an oligonucleotide array (I) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX different capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX and contacting the modified target nucleic acid with (I). The steps of
XX above method is useful for detecting a target nucleic acid, which further
XX comprises detecting the presence of the modified target nucleic acid

XX
XX SQ Sequence 24 BP; 6 A; 5 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 67.0%; Score 13.4; DB 6; Length 24;
Best Local Similarity 93.3%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 TTCGAGGAGCGGCT 20

Db 6 TGGCAGGAGCGGCT 20

RESULT 22

AAZ89440

ID AAZ89440 standard; DNA; 23 BP.

XX AAZ89440;
 AC 15-JUN-2000 (first entry)
 DT Human type IV collagen alpha-3 chain primer #40.
 DE
 XX
 DE Human; primer; immunogenic; alpha-3 chain; type IV collagen; therapy;
 KW autoantibody; Goodpasture's syndrome; immunosuppression; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200011475-A1.
 PN
 XX 02-MAR-2000.
 PD
 XX 20-AUG-1999; 99WO-SE001416.
 PF
 XX 21-AUG-1998; 98SE-00002788.
 PR
 XX (WIES-) WIESLAB AB.
 PA
 XX Wieslander J, Hellmark T;
 PI
 XX WPI; 2000-246583/21.
 DR
 XX Novel immunogenic region recognized by autoantibodies from goodpasture's
 PT patients for detecting their presence in circulating body fluid comprises
 PT a non-collagenous approximately a3 chain domain of type IV collagen.
 PT
 XX Example; Page 13; 36pp; English.
 PS
 XX This invention describes a novel immunogenic region (I) comprising an
 CC epitope of non-collagenous alpha-3 chain domain of type IV collagen which
 CC has intact cysteine residues. The epitope is located in the amino
 CC terminal end of alpha3 chain and is recognized by circulating
 CC autoantibodies (A) from a Goodpasture's patient. The product of the
 CC invention has immunosuppressive activity, blocks autoantibodies and kills
 CC cells producing (A) with an epitope-toxin complex. (I) is used for in
 CC vitro determination of (A) in a body fluid by contacting it with the
 CC immunogenic polypeptide molecule or a recombinant nucleic acid and
 CC determining antigen-antibody reaction by physical or chemical method. The
 CC determination can also be done by contacting the body fluid with anti-
 CC idiotypic antibodies and determining antigen-antibody reaction by
 CC physical or chemical methods. (I) is also used in therapy for treating
 CC Goodpasture's syndrome. AAZ89401-289440 represent primers used in the
 CC isolation of the products of the invention
 CC
 XX Sequence 23 BP; 4 A; 6 C; 7 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 66.0%; Score 13.2; DB 3; Length 23;
 ID Best Local Similarity 83.3%; Pred. No. 1.5e+04;
 XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 AC
 XX 2 ACTCTTGACGAGGCGGC 19
 DT ||| ||||| |||||
 DE 6 ACTTTTGACGAGCAGTCG 23
 XX
 RESULT 23
 ADH72962
 ID ADH72962 standard; DNA; 25 BP.
 XX
 AC ADH72962;
 DT 25-MAR-2004 (first entry)
 DE
 XX M. tuberculosis capture oligonucleotide #70.
 DE
 XX ss; single nucleotide polymorphism; SNP detection; genotyping;
 KW pathogen detection; pathogen identification.
 KW
 XX Mycobacterium tuberculosis.
 OS

XX US2003232341-A1.
 PN 18-DEC-2003.
 PD
 XX 12-JUN-2002; 2002US-00170332.
 PF
 XX 12-JUN-2002; 2002US-00170332.
 PR
 XX (CASE/) CASEY W M.
 PA (CHEN/) CHEN J.
 PA (COLT/) COLTON H M.
 PA (TAYL/) TAYLOR J D.
 PA (WEIN/) WEINER M P.
 XX
 XX Casey WM, Chen J, Colton HM, Taylor JD, Weiner MP;
 PI WPI; 2004-052156/05.
 DR
 XX Detecting single nucleotide polymorphisms in target nucleic acids, useful
 PT for e.g. in genotyping or in pathogen detection and identification,
 PT comprises detecting the labels in the hybridization products.
 PT
 XX Claim 1; SEQ ID NO 124; 60pp; English.
 PS
 XX The invention relates to a method of detecting a result from an
 CC identification reaction to identify a selected nucleotide in a target
 CC nucleic acid comprising detecting the label of the labelled detection
 CC product in the hybridisation products, the presence of the label
 CC indicating the identity of the selected nucleotide in the target nucleic
 CC acid. The method is useful for rapid detection of single nucleotide
 CC polymorphisms in a nucleic acid sample. These may be used for genotyping
 CC (such as for disease mutation detection and for parentage determinations
 CC in humans and other animals), pathogen detection and identification and
 CC differential gene expression. The present sequence represents a
 CC Mycobacterium tuberculosis capture oligonucleotide.
 XX
 SQ Sequence 25 BP; 5 A; 9 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 66.0%; Score 13.2; DB 12; Length 25;
 ID Best Local Similarity 83.3%; Pred. No. 1.5e+04;
 XX Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 AC
 XX 3 CTCTTTCAGGATACGGCT 20
 DT ||||| ||||| |||||
 DE 7 CTCTTTCAGGATACGGCT 24
 XX
 RESULT 24
 AAF46591/C
 ID AAF46591 standard; DNA; 15 BP.
 XX
 AC AAF46591;
 XX 30-MAR-2001 (first entry)
 DT
 XX IGFBP3 oligonucleotide #11.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX

```

PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX
XX WPI; 2001-041421/05.
XX
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX Example 7; Page 44; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
XX Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 65.0%; Score 13; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GCAGGAAGCGGCT 20
DB 13 GCAGGAAGCGGCT 1
|||||
|

RESULT 25
AAF46590/c
ID AAF46590 standard; DNA; 15 BP.
XX
XX AAF46590;
AC
XX 30-MAR-2001 (first entry)
DT
XX IGFBP3 oligonucleotide #10.
DE
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX
XX

```


DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 7; Page 44; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAP45151 and AAP45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 65.0%; Score 13; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 GCAGGAAGCGGCT 20
| | | | | | | | | |
Db 15 GCAGGAAGCGGCT 3
RESULT 27
ID ADP14476 standard; DNA; 25 BP.
XX
AC ADP14476;
XX
DT 26-AUG-2004 (first entry)
XX
DE Renal cell carcinoma differentially expressed gene probe #881.
XX
KW ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
OS Homo sapiens.
XX
PN WO2004048933-A2.
XX
PD 10-JUN-2004.
XX
PF 21-NOV-2003; 2003WO-US037481.
XX
PR 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX
PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
DR WPI; 2004-460799/43.
XX
XX Diagnosing non-blood disease such as solid tumor, involves comparing
XX differential expression profile of specific genes in peripheral blood
XX sample of subject with reference expression profile of specific genes.
XX
PS Disclosure; SEQ ID NO 1212; 350pp; English.
XX
CC The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
SQ Sequence 25 BP; 8 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 TCTTGCGAGGAAGC 16
| | | | | | | | | |
Db 6 TCTTGCGAGGAAGC 18
RESULT 28
ABS59220
ID ABS59220 standard; DNA; 26 BP.
XX
AC ABS59220;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human G-protein coupled receptor, probe #123.
XX
KW Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis;
KW diabetes; cell signal processing; metabolic pathway modulation; cancer;
KW adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma;
KW immune response; neurodegenerative disorder; inflammatory disorder;
KW Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy;
KW probe; ss.
XX
OS Homo sapiens.
XX
PN WO200259313-A2.
XX
PD 01-AUG-2002.
XX
PF 18-DEC-2001; 2001WO-US049394.
XX
PR 18-DEC-2000; 2000US-0256635P.
PR 21-DEC-2000; 2000US-0257876P.
PR 04-JAN-2001; 2001US-0259743P.
PR 10-JAN-2001; 2001US-0260718P.
PR 12-JAN-2001; 2001US-0261498P.
PR 24-JAN-2001; 2001US-0263689P.
PR 08-FEB-2001; 2001US-0267464P.
PR 22-FEB-2001; 2001US-0271021P.
PR 14-MAR-2001; 2001US-0275946P.
PR 23-MAR-2001; 2001US-0278150P.
PR 18-APR-2001; 2001US-0284591P.
PR 23-APR-2001; 2001US-0285718P.
PR 19-JUN-2001; 2001US-0299327P.

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PR 16-AUG-2001; 2001US-0312902P.
XX (CURA-) CURAGEN CORP.
PA
XX Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA;
XX Caaman SJ, Vernet CAM, Shenoy SG, Gusev V, Malyankar UM, Edinger S;
XX Gerlach V, Smithson G, Stone D, Sciore P, Macdougall JR, Gunther E;
XX Peyman JA, Ellerman K, Gangolli EA, Millet I;
XX WPI; 2002-599789/64.
XX
XX New G protein coupled receptor polypeptides and polynucleotides, useful
XX in gene therapy, particularly for treating or preventing cardiomyopathy,
XX atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
XX in humans.
XX
XX Claim 1; Page 652; 685pp; English.
XX
XX The invention relates to novel isolated G-protein coupled receptor (GPCR)
XX polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
XX and antibody are useful for treating, preventing or alleviating a GPCR-
XX associated disorder or a pathological state in a subject, particularly a
XX human. In particular, the disorder is cardiomyopathy, atherosclerosis,
XX diabetes, or a disorder related to cell signal processing and metabolic
XX pathway modulation. The GPCR polypeptide and nucleic acid are also useful
XX for diagnosing the presence of or predisposition to a disease associated
XX with altered levels of GPCR, particularly cancer. The GPCR nucleic acid
XX and polypeptide are especially useful in therapeutic or prophylactic
XX applications for disorders associated with aberrant GPCR expression or
XX activity. The DNA encoding the protein is useful in gene therapy for
XX treating the above conditions. Furthermore, the nucleic acids and
XX polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
XX cancer, uterus cancer, immune response, neurodegenerative disorders,
XX asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
XX Alzheim hereditary osteodysrophy. These are also useful in developing a
XX powerful assay system for functional analysis of various human disorders,
XX as well as in diagnostic applications. ABS58747-ABS59231 represent human
XX GPCR coding sequences, primers and probes of the invention
XX
XX Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 65.0%; Score 13; DB 6; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+04;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 4 TCTTGCAGGAAGC 16
XX | | | | | | | |
XX 3 TCTTGCAGGAAGC 15
XX
XX RESULT 29
XX ABT04530
XX ID ABT04530 standard; DNA; 26 BP.
XX AC ABT04530;
XX
XX 25-SEP-2002 (first entry)
XX
XX Human G-protein coupled receptor probe SEQ ID NO: 473.
XX
XX Human; G-protein coupled receptor; GPCR; developmental disease;
XX immune disease; retinal disease; metabolic disorder; feeding disorder;
XX wasting disorder; infection; cancer; allergy; neurological disorder;
XX behavioural disorder; reproductive disorder; antidiabetic; cardiant;
XX antiatherosclerotic; probe; ss.
XX
XX Homo sapiens.
XX
XX WO200255558-A2.
XX
XX 18-JUL-2002.
XX
XX 18-DEC-2001; 2001WO-US049112.
XX
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XX 18-DEC-2000; 2000US-0256635P.
XX 21-DEC-2000; 2000US-0257876P.
XX 04-JAN-2001; 2001US-0259743P.
XX 10-JAN-2001; 2001US-0260718P.
XX 12-JAN-2001; 2001US-0261498P.
XX 24-JAN-2001; 2001US-0263689P.
XX 08-FEB-2001; 2001US-0267464P.
XX 22-FEB-2001; 2001US-0271021P.
XX 14-MAR-2001; 2001US-0275946P.
XX 23-MAR-2001; 2001US-0278150P.
XX 18-APR-2001; 2001US-0284591P.
XX 23-APR-2001; 2001US-0285718P.
XX 19-JUN-2001; 2001US-0299327P.
XX 16-AUG-2001; 2001US-0312902P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Padigaru M, Kekuda R, Li L, Ballinger RA, Casman SJ, Spytek KA;
XX Colman SD, Vernet CAM, Shenoy S, Gusev V, Malyankar UM, Edinger S;
XX Gerlach V, Smithson G, Stone D, Sciore P, Macdougall JR, Gunther E;
XX Peyman JA, Ellerman K, Millet I, Tchervnev VT, Anderson DW, Wolenc A;
XX WPI; 2002-500840/53.
XX
XX New G-protein coupled receptor polypeptides, encoding nucleic acids and
XX immunospecific antibodies, useful for treating cardiomyopathy,
XX atherosclerosis, diabetes or disorder related to cell signal processing
XX and metabolic pathway modulation.
XX
XX Example 3; Page 457; 473pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX G-protein coupled receptors designated GPCRXX. These can be used in the
XX treatment of developmental diseases, immune diseases, retinal diseases,
XX metabolic disorders, feeding disorders, wasting disorders, infections,
XX cancer, allergies, neurological disorders, behavioural disorders and
XX reproductive disorders. The present sequence is a probe used to isolate a
XX coding sequence of the invention. The sequence is modified at the 5' end
XX by TET and at the 3' end by FAMRA
XX
XX Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 65.0%; Score 13; DB 6; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+04;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 4 TCTTGCAGGAAGC 16
XX | | | | | | | |
XX 3 TCTTGCAGGAAGC 15
XX
XX RESULT 30
XX ABT05715
XX ID ABT05715 standard; DNA; 26 BP.
XX
XX AC ABT05715;
XX
XX 16-OCT-2002 (first entry)
XX
XX GPCR related probe SEQ ID No 168.
XX
XX Antidiabetic; cytostatic; anorectic; nootropic; neuroprotective; GPCRX;
XX antiparkinsonian; cardiant; antiarteriosclerotic; immunosuppressive;
XX hypotensive; haemostatic; antifertility; antiasthmatic; antiinflammatory;
XX anti-HIV; G-protein coupled receptor X; cardiomyopathy; atherosclerosis;
XX diabetes; metabolic disorder; diabetes; obesity; infectious disease;
XX anorexia; neurodegenerative disorder; Alzheimer's disease; dyslipidaemia;
XX Parkinson's disorder; immune disorder; haematopoietic disorder; obesity;
XX metabolic syndrome X; wasting disorder; cancer; hypertension; neoplasia;
XX congenital heart defect; aortic stenosis; subaortic stenosis; lymphoma;
XX transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;
XX prostate cancer; adenocarcinoma; uterus cancer; fertility; haemophilia;
```

KW hypercoagulation; idiopathic thrombocytopenic purpura; immunodeficiency;
KW graft versus host disease; AIDS; bronchial asthma; Crohn's disease;
KW multiple sclerosis; chromosome mapping; tissue typing; forensic biology;
KW gene therapy; transgenic animal; probe; ss.

XX Unidentified.

XX WO200246229-A2.

XX 13-JUN-2002.

XX 05-DEC-2001; 2001WO-US046530.

XX 05-DEC-2000; 2000US-0251459P.

XX 29-DEC-2000; 2000US-0259007P.

XX 04-DEC-2001; 2001US-00005041.

XX (CURA-) CURAGEN CORP.

XX Casman SJ, Padigar M, Burgess CE, Shimkets RA, Spytek KA;

PI Gilbert JA, Mayotte JE, Baumgartner JC, Mishra V, Vernet CAM;

PI Dickinson KS, Ballinger RA, Wolenc AR;

XX WPI; 2002-537559/57.

XX Novel isolated G-protein coupled receptor polypeptide, designated NOVX,
PT useful for treating or preventing human receptor-associated disorders
PT e.g. cardiomyopathy, atherosclerosis or diabetes.

XX Example 2; Page 221; 264pp; English.

XX The invention relates to a novel isolated G-protein coupled receptor X
CC (GPCR) polypeptide. The isolated protein, its encoding polynucleotide
CC and the antibody of the isolated protein is useful for treating or
CC preventing a GPCR-associated disorder in a subject, preferably human,
CC where the disorder is cardiomyopathy, atherosclerosis or diabetes. The
CC isolated protein, its encoding polynucleotide and the antibody of the
CC isolated protein is useful for treating or preventing metabolic
CC disorders, diabetes, obesity, infectious disease, anorexia,
CC neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder,
CC immune disorders, hematopoietic disorders, and various dyslipidaemias,
CC metabolic disturbances associated with obesity, the metabolic syndrome X,
CC wasting disorders associated with chronic diseases, and cancer. The
CC disorders also include cardiomyopathy, atherosclerosis, hypertension,
CC congenital heart defects, aortic stenosis, subaortic stenosis,
CC transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia,
CC prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer,
CC fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic
CC purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial
CC asthma, Crohn's disease, and multiple sclerosis. The isolated protein,
CC its encoding polynucleotide and the antibody of the isolated protein is
CC useful in screening assays, detection assays (e.g., chromosomal mapping,
CC tissue typing, forensic biology). The isolated polynucleotide is useful
CC in gene therapy, to express the isolated protein, to detect GPCR mRNA or
CC a genetic lesion in a GPCR gene, and to modulate GPCR activity. The
CC cell of the invention is useful for producing non-human transgenic
CC animals. This polynucleotide sequence represents a probe of a GPCR
CC protein of the invention

XX Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 65.0%; Score 13; DB 6; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.9e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGC 16

DB 3 TCTTGCAGGAGC 15

|||||

RESULT 31

ADH31280

ID ADH31280 standard; DNA; 26 BP.

XX ADH31280;

XX 11-MAR-2004 (first entry)

XX Human G-protein coupled receptor (GPCR) cDNA probe #107.

XX Human; G-protein coupled receptor; GPCR; ss; GPCR; cardiomyopathy;
XX atherosclerosis; diabetes; obesity; infection; cancer;
XX Alzheimer's disease; Parkinson's disease; asthma; allergy; hypertension;
XX retinal disease; urinary retention; angina pectoris; Crohn's disease;
XX schizophrenia; manic depression; probe.

XX Homo sapiens.

XX OS

XX US2003232332-A1.

XX 18-DEC-2003.

XX 18-DEC-2001; 2001US-00024212.

XX 18-DEC-2000; 2000US-0256635P.

XX 21-DEC-2000; 2000US-0257876P.

XX 04-JAN-2001; 2001US-0259743P.

XX 10-JAN-2001; 2001US-0260718P.

XX 12-JAN-2001; 2001US-0261498P.

XX 24-JAN-2001; 2001US-0263689P.

XX 08-FEB-2001; 2001US-0267464P.

XX 22-FEB-2001; 2001US-0271021P.

XX 14-MAR-2001; 2001US-0275946P.

XX 23-MAR-2001; 2001US-0278150P.

XX 18-APR-2001; 2001US-0284591P.

XX 23-APR-2001; 2001US-0285718P.

XX 19-JUN-2001; 2001US-0299327P.

XX 16-AUG-2001; 2001US-0312902P.

XX (PADI/) PADIGARU M.

XX (KEKU/) KEKUDA R.

XX (LILL/) LI L.

XX (BALL/) BALLINGER R A.

XX (CASM/) CASMAN S J.

XX (SPYT/) SPYTEK K A.

XX (COLM/) COLMAN S D.

XX (VERN/) VERNET C A M.

XX (SHEN/) SHENOY S G.

XX (GUSE/) GUSEV V Y.

XX (MALY/) MALYANKAR U M.

XX (EDIN/) EDINGER S R.

XX (GERL/) GERLACH V.

XX (SMIT/) SMITHSON G.

XX (STON/) STONE D J.

XX (SCIO/) SCIORE P.

XX (MACD/) MACDOUGALL J R.

XX (GUNT/) GUNTHER E.

XX (PEYM/) PEYMAN J A.

XX (ELLE/) ELLERMAN K.

XX (MILL/) MILLET I.

XX (TCHE/) TCHERNEV V T.

XX (ANDE/) ANDERSON D W.

XX (WOLE/) WOLENC A R.

XX

XX Padigar M, Kekuda R, Li L, Ballinger RA, Casman SJ, Spytek KA;

PI Colman SD, Vernet CAM, Sheno S G, Gusev VY, Malyankar UM;

PI Edinger SR, Gerlach V, Smithson G, Stone DJ, Scioire P;

PI Macdougall JR, Gunther E, Peyman JA, Ellerman K, Millet I;

PI Tchernev VT, Anderson DW, Wolenc AR;

XX WPI; 2004-061267/06.

XX New G-protein coupled receptor (GPCR) polypeptides and nucleic acids,
PT useful for diagnosing, preventing or treating GPCR-associated disorders,
PT e.g. cardiomyopathy, atherosclerosis or diabetes, and in
PT pharmacogenomics.

XX PS Example 3; SEQ ID NO 472; 328pp; English.

XX CC The invention relates to human G-protein coupled receptor (GPCR)

XX CC polypeptides and the polynucleotides encoding them, designated GPCRXX. The

XX CC invention also relates to a vector comprising a GPCRXX nucleic acid, a

XX CC cell comprising the vector, an antibody that binds immunospecifically to

XX CC a GPCRXX polypeptide, methods for determining the presence or amount of

XX CC the polypeptide or the nucleic acid molecule in a sample, methods for

XX CC identifying an agent that binds to or modulates the expression or

XX CC activity of a polypeptide and a method for modulating the activity of the

XX CC polypeptide. The composition and methods are useful in diagnosing,

XX CC preventing or treating GPCRXX-associated disorders, such as

XX CC cardiomyopathy, atherosclerosis, diabetes, obesity, infections, cancer,

XX CC Alzheimer's disease, Parkinson's disease, asthma, allergies,

XX CC hypertension, retinal diseases, urinary retention, angina pectoris,

XX CC Crohn's disease, schizophrenia and manic depression. The nucleic acids

XX CC are further used as hybridisation probes, in chromosome mapping, tissue

XX CC typing, preventive medicine and pharmacogenomics. The polypeptides are

XX CC also useful as vaccines or as immunogens to produce antibodies. This

XX CC sequence represents a probe which hybridises to human GPCRXX cDNA of the

XX CC invention.

XX SQ Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 65.0%; Score 13; DB 12; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.9e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGC 16

Db 3 TCTTGCAGGAAGC 15

RESULT 32

ADK98351/c

ID ADK98351 standard; DNA; 24 BP.

XX AC ADK98351;

XX DT 06-MAY-2004 (first entry)

XX XX Primer of the invention #4071.

XX DE human; single nucleotide polymorphism; SNP; ss; primer.

XX KW Synthetic.

XX OS JP2003259875-A.

XX PN 16-SEP-2003.

XX PD 08-MAR-2002; 2002JP-00064373.

XX PF 08-MAR-2002; 2002JP-00064373.

XX PR (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX PA WPI; 2004-093977/10.

XX DR Novel polynucleotide useful for PCR amplification along with two DNA

XX PT fragment from another set of sequences, or for detecting single

XX PT nucleotide polymorphism in human gene.

XX XX Claim 2; SEQ ID NO 7380; 2627pp; Japanese.

XX CC The present invention relates to a polynucleotide isolated from a human

XX CC gene and is useful for detecting a single nucleotide polymorphism in a

XX CC human gene or for diagnosing of disease. The invention enables the

XX CC detection of a single nucleotide polymorphism in a human gene. The

XX CC present sequence represents a primer of the invention.

XX SQ Sequence 24 BP; 5 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 9; Length 25;

Best Local Similarity 87.5%; Pred. No. 2.4e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAGC 16

Db 19 GACTCTAGCAGGCAGC 4

RESULT 33

ACII12520

ID ACII12520 standard; DNA; 25 BP.

XX AC ACII12520;

XX DT 13-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 12511.

XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;

XX KW genetic variation; biallelic marker; polymorphism; human;

XX KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX DR WPI; 2003-567953/53.

XX PT New array of nucleic acid probes, useful for in situ hybridization, in

XX PT Southern, Northern or dot-blot hybridization to identify or detect the

XX PT sequence or specific mutations of any gene.

XX PS Claim 1; SEQ ID NO 12511; 9pp; English.

XX CC The invention discloses a microarray comprising a plurality of nucleic

XX CC acid probes including one of 2,018,500 fully defined sequences, or its

XX CC perfect match, perfect mismatch, antisense match or antisense mismatch.

XX CC Also disclosed is a method of gene expression analysis. The array is used

XX CC in monitoring gene expression levels by hybridisation to a DNA library,

XX CC in analysis of genetic variation or in hybridisation of tag-labelled

XX CC compounds. The nucleic acid probes are specifically designed for analysis

XX CC of at least one target sequence. The method of analysis comprises

XX CC hybridising at least one or more nucleic acids to at least two or more

XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid

XX CC probes are attached to a solid support. The analysis comprises monitoring

XX CC gene expression levels, identifying biallelic markers or polymorphisms,

XX CC or family members of a gene and a cross-species comparison. Each of the

XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid

XX CC probes is useful in situ hybridisation, in Southern, Northern or dot-

XX CC blot hybridisation to identify or detect the sequence or specific

XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by

XX CC primer extensions or in screening cDNA or genomic libraries or subclones

XX CC for additional subclones containing segments of DNA that have been

XX CC isolated and previously sequenced. The sequence presented is one of the

XX CC nucleic acid probes incorporated in the microarray. Note: The sequence

XX CC data for this patent can also be obtained in electronic format directly

XX CC from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 11 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

```
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAGCG 16
   |||||
DB 1 GACTCATGAGGAGCG 16

RESULT 34
ACH63464
ID ACH63464 standard; DNA; 25 BP.
AC ACH63464;
XX
XX 17-OCT-2003 (first entry)
XX
XX DNA target sequence #12600 useful in array for genetic analyses.
XX
XX Gene expression analysis; array; hybridisation; genetic variation;
XX tag-labelled compound; gene family; in situ hybridisation;
XX library screening; Southern hybridisation; northern hybridisation;
XX dot-blot hybridisation; gene sequence; mutation detection;
XX target sequence; probe; PCR; primer; ss.
XX
XX Unidentified.
XX
XX US2003082596-A1.
XX
XX 01-MAY-2003.
XX
XX 08-AUG-2002; 2002US-00215112.
XX
XX 08-AUG-2001; 2001US-0311040P.
XX (MITT/) MITTMANN M.
XX Mittmann M;
XX WPI; 2003-576608/54.
XX
XX New probe array useful e.g. for monitoring gene expression levels, for
XX analysing genetic variations, or for hybridizing tag-labeled compounds,
XX comprises multiple nucleic acid probes.
XX
XX Claim 1; SEQ ID NO 12600; 9pp; English.
XX
XX The present invention relates to nucleic acid sequences that are
XX complementary to particular genes, and can be used as probes for a
XX variety of analyses such as gene expression analysis. Each probe
XX comprises 9 or more consecutive nucleotides from at least one of 14936
XX nucleotide sequences defined in the patent, or their perfect sense match,
XX sense mismatch, antisense match or antisense mismatch oligonucleotides.
XX The probes may be used in an array comprising at least 10 distinct
XX nucleic acid probes. The array is useful in monitoring gene expression
XX levels by hybridisation to a DNA library, in analysing genetic
XX variations, and in hybridising tag-labelled compounds. The probes are
XX useful for identifying family members of a gene. The probes are also
XX useful in situ hybridisations, in screening cDNA or genomic libraries
XX (or derived subclones) for additional clones containing segments of DNA
XX that have been previously isolated and sequenced, in Southern, northern,
XX or dot-blot hybridisation of genomic DNA to identify or detect the
XX sequence of any gene or detect specific mutations in any gene, and in
XX mapping the 5' termini of mRNA molecules by primer extensions. The
XX nucleic acid sequences of the invention are also useful as PCR primers.
XX The invention provides a large collection of nucleic acid sequences
XX complementary to particular genes with a wide range of analytical uses.
XX ACH50865-ACH5260 represent the target sequences of the invention. Note:
XX The sequence data for this patent was obtained in electronic format
XX directly from the USPTO web site at seqdata.uspto.gov/psipsiDentry.html
XX
XX Sequence 25 BP; 8 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 9; Length 25;

Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAGCG 17
   |||||
DB 9 ACTTTGCAGGAGCG 24

RESULT 35
ACH51423
ID ACH51423 standard; DNA; 25 BP.
XX
XX ACH51423;
XX
XX 16-OCT-2003 (first entry)
XX
XX DNA target sequence #559 useful in array for genetic analyses.
XX
XX Gene expression analysis; array; hybridisation; genetic variation;
XX tag-labelled compound; gene family; in situ hybridisation;
XX library screening; Southern hybridisation; northern hybridisation;
XX dot-blot hybridisation; gene sequence; mutation detection;
XX target sequence; probe; PCR; primer; ss.
XX
XX Unidentified.
XX
XX US2003082596-A1.
XX
XX 01-MAY-2003.
XX
XX 08-AUG-2002; 2002US-00215112.
XX
XX 08-AUG-2001; 2001US-0311040P.
XX (MITT/) MITTMANN M.
XX Mittmann M;
XX WPI; 2003-576608/54.
XX
XX New probe array useful e.g. for monitoring gene expression levels, for
XX analysing genetic variations, or for hybridizing tag-labeled compounds,
XX comprises multiple nucleic acid probes.
XX
XX Claim 1; SEQ ID NO 559; 9pp; English.
XX
XX The present invention relates to nucleic acid sequences that are
XX complementary to particular genes, and can be used as probes for a
XX variety of analyses such as gene expression analysis. Each probe
XX comprises 9 or more consecutive nucleotides from at least one of 14936
XX nucleotide sequences defined in the patent, or their perfect sense match,
XX sense mismatch, antisense match or antisense mismatch oligonucleotides.
XX The probes may be used in an array comprising at least 10 distinct
XX nucleic acid probes. The array is useful in monitoring gene expression
XX levels by hybridisation to a DNA library, in analysing genetic
XX variations, and in hybridising tag-labelled compounds. The probes are
XX useful for identifying family members of a gene. The probes are also
XX useful in situ hybridisations, in screening cDNA or genomic libraries
XX (or derived subclones) for additional clones containing segments of DNA
XX that have been previously isolated and sequenced, in Southern, northern,
XX or dot-blot hybridisation of genomic DNA to identify or detect the
XX sequence of any gene or detect specific mutations in any gene, and in
XX mapping the 5' termini of mRNA molecules by primer extensions. The
XX nucleic acid sequences of the invention are also useful as PCR primers.
XX The invention provides a large collection of nucleic acid sequences
XX complementary to particular genes with a wide range of analytical uses.
XX ACH50865-ACH5260 represent the target sequences of the invention. Note:
XX The sequence data for this patent was obtained in electronic format
XX directly from the USPTO web site at seqdata.uspto.gov/psipsiDentry.html
XX
XX Sequence 25 BP; 7 A; 4 C; 9 G; 5 T; 0 U; 0 Other;
```

```
Best Local Similarity 87.5%; Pred. NO. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGCGGC 19
Db 2 TCTTGAAGGAAGTGGC 17

RESULT 36
ACH53400
ID ACH53400 standard; DNA; 25 BP.
XX
AC ACH53400;
XX
DT 16-OCT-2003 (first entry)
XX
DE DNA target sequence #2536 useful in array for genetic analyses.
XX
KW Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
PN US2003082596-A1.
XX
PD 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
XX
PA (MITT/) MITTMANN M.
XX
PI Mittmann M;
XX
WPI; 2003-576608/54.
XX
New probe array useful e.g. for monitoring gene expression levels, for
PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
XX
Claim 1; SEQ ID NO 2536; 9pp; English.
XX
The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/paipsDIDEntry.html
XX
SQ Sequence 25 BP; 6 A; 5 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. NO. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTTGCAGGAGCGGCT 20
Db 8 CTTGCAGGAGCGGCT 23

Best Local Similarity 87.5%; Pred. NO. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACTCTTGCGAGGACCG 17
Db 3 ACTTTTGCGAGGACCG 18

RESULT 37
AAX22793
ID AAX22793 standard; DNA; 27 BP.
XX
AC AAX22793;
XX
DT 27-MAY-1999 (first entry)
XX
DE PCR primer 84672.
XX
KW Protein-enveloped polyribonucleic acid; viral RNA; bacteriophage RNA;
KW diagnostic; detection; assay; PCR primer; ss.
XX
OS Synthetic.
XX
DE19737442-A1.
XX
PN 04-MAR-1999.
XX
PF 22-AUG-1997; 97DE-01037442.
XX
PR 22-AUG-1997; 97DE-01037442.
XX
PA (OLFEB-) OLFERT LANDT TIB MOLBIOL SYNTHESLABOR.
XX
PI Landt O;
XX
WPI; 1999-168279/15.
XX
Genetically modified RNA viruses or bacteriophages - useful as RNA
XX standards, positive controls, etc.
XX
Example 5; Col 15; 12pp; German.
XX
This invention describes protein-enveloped polyribonucleic acids
CC containing viral RNA or bacteriophage RNA, characterised in that the
CC natural nucleic acid sequence is varied. Also described is a method for
CC producing a protein-enveloped polyribonucleic acid. Protein-enveloped
CC polyribonucleic acids are useful as standards for diagnostic methods in
CC which the presence of a specific ribonucleic acid is detected, and are
CC useful as standard or competitor sequences for methods in which the
CC amount of a defined ribonucleic acid is determined. They are also useful
CC as positive controls for the detection of viral RNA, where the protein-
CC enveloped polyribonucleic acid is added directly to the assay sample and
CC is isolated in parallel with the viral RNA. They can monitor the
CC efficiency of processes for purifying nucleic acids or the efficiency of
CC the reverse transcription of ribonucleic acids, and are useful a
CC comparison substances in assays in which nucleic acids are detected by
CC hybridisation or in assays in which nucleic acids are detected after or
CC during nucleic acid amplification. They are useful as carriers for RNA
CC sequences having a functional property, and for mixtures of RNA sequences
CC from which individual RNA sequences can be selected
XX
SQ Sequence 27 BP; 9 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 2; Length 27;
Best Local Similarity 87.5%; Pred. NO. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

RESULT 38

ADCS1654
ID ADCS1654 standard; DNA; 27 BP.
AC
XX
AC ADCS1654;
XX
DT 18-DEC-2003 (first entry)
XX
DE 5' PCR primer to amplify human soluble transferrin receptor (stfr) cDNA.
XX
KW Human; ss; PCR; primer; bioengineering process;
XX KW soluble type transferrin receptor; stfr; iron saturated transferrin;
XX KW transferrin receptor.
XX
OS Homo sapiens.
XX
PN JP2002369687-A.
XX
PD 24-DEC-2002.
XX
PF 18-MAY-2001; 2001JP-00148698.
XX
PR 02-MAR-2001; 2001JP-00057780.
XX
PA (BIKE) EIKEN KAGAKU KK.
XX
DR WPI; 2003-472838/45.
XX
PT A bioengineering safe, low cost and mass production process of a soluble
XX PT type transferrin receptor (stfr) used as markers of cancer and
XX PT hematopoietic function.
XX
PS Example 3; Page 4; 9pp; Japanese.
XX
CC The invention discloses a bioengineering process for the preparation of a
XX CC soluble type transferrin receptor (stfr). The process comprises the
XX CC preparation of a DNA encoding for an amino acid sequence of stfr,
XX CC preparation of a recombinant DNA by insertion of the DNA in a vector
XX CC (e.g. a vector containing a signal sequence, particularly an
XX CC immunoglobulin sequence), transformation of the recombinant DNA in host
XX CC cells, culture of the transformed host cells to produce stfr and
XX CC purification and collection of the produced stfr. Optionally, further
XX CC treatment of the collected stfr with an excess amount of iron saturated
XX CC transferrin, to give a complex, followed by purification of the complex,
XX CC particularly by an anionic ion exchange column, used for determination of
XX CC transferrin receptor in a living sample using the recombinant stfr as a
XX CC standard, can be carried out. The inventive process is safe, low cost and
XX CC is useful for mass production of stfr. The sequence presented is a PCR
XX CC primer which was used to amplify human stfr cDNA.
XX
SQ Sequence 27 BP; 7 A; 7 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 64.0%; Score 12.8; DB 10; Length 27;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 ACTCTTGCGAGGACCG 17
|||||
Db 6 ACTCTTGCGAGGACCG 21
RESULT 39
ABZ21923
ID ABZ21923 standard; DNA; 30 BP.
XX
AC ABZ21923;
XX
DT 28-MAR-2003 (first entry)
XX
DE Mouse fusion protein dimer related PCR primer SEQ ID NO:14.
XX
KW Mouse; prion protein dimer; fusion protein; vaccination; vaccine;
XX KW prion protein; virucide; immunostimulant; spongiform encephalopathy;
XX KW transmissible spongiform encephalopathy; PCR primer; ss.

XX
OS Mus sp.
XX OS Synthetic.
XX
PN EP1251138-A1.
XX
PD 23-OCT-2002.
XX
PF 19-APR-2001; 2001EP-00109707.
XX
PR 19-APR-2001; 2001EP-00109707.
XX
PA (SCHA/) SCHAETZL H.
XX
XX Schaeztl H;
XX
XX WPI; 2003-095100/09.
XX
XX New prion protein dimer, useful as a vaccine against spongiform
XX PT encephalopathy.
XX
PS Example 1; Page 6; 23pp; English.
XX
CC The present invention describes a prion protein which is a homodimer or
XX CC heterodimer (I). Also described: (1) an antibody which specifically binds
XX CC the protein; (2) a DNA sequence encoding the protein; and (3) an
XX CC expression vector containing the DNA. (1) has virucide and
XX CC immunostimulant activities. The protein can be used for producing for
XX CC antibodies, and the protein, antibody, DNA and vector are useful for
XX CC preparing a vaccine for preventing or treating a transmissible spongiform
XX CC encephalopathy. There is no current vaccine for spongiform
XX CC encephalopathies. The present sequence represents a PCR primer used in
XX CC the generation of a fusion prion protein dimer in an example from the
XX CC present invention
XX
SQ Sequence 30 BP; 9 A; 6 C; 10 G; 5 T; 0 U; 0 Other;
Query Match 64.0%; Score 12.8; DB 10; Length 30;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 TCTTGCGAGGAGCGGC 19
|||||
Db 10 TCTTGCGAGGAGCGGC 25
RESULT 40
ADM92376/C
ID ADM92376 standard; DNA; 20 BP.
XX
AC ADM92376;
XX
DT 01-JUL-2004 (first entry)
XX
DE Pancreatic cancer related RT-PCR forward primer SEQ ID NO:13.
XX
XX Pancreatic cancer; diagnosis; pancreatic cancer-associated gene;
XX KW cytostatic; vaccine; gene therapy; human; reverse transcription; PCR;
XX KW primer; ss; semi-quantitative RT-PCR experiment.
XX
OS Homo sapiens.
XX OS Synthetic.
XX
PN WO2004031412-A2.
XX
PD 15-APR-2004.
XX
PF 17-SEP-2003; 2003WO-JP011817.
XX
PR 30-SEP-2002; 2002US-0414872P.
XX PR 28-FEB-2003; 2003US-0450889P.
XX
XX (ONCO-) ONCOTHERAPY SCI INC.

(UITY) UNIV TOKYO.

Nakamura Y, Katagiri T;
WPI; 2004-330205/30.

Diagnosing pancreatic cancer (PNC) comprises determining a level of
expression of a PNC-associated gene in a patient derived biological
sample.

Example 1; SEQ ID NO 13; 152bp; English.

The present invention describes a method for diagnosing pancreatic cancer
(PNC) or a predisposition to developing PNC in a subject. The method
comprises determining a level of expression of a PNC-associated gene in a
patient derived biological sample, where an increase or decrease of the
level compared to a normal control level of the gene indicates that the
subject suffers from or is at risk of developing PNC. Also described: (1)
a PNC reference expression profile, comprising a pattern of gene
expression of two or more genes, i.e. PNC 1-605 or PNC 850-866 and PNC
894-906; (2) a method of screening for a compound for treating or
preventing PNC or malignant PNC; (3) a kit comprising a detection reagent
which binds to two or more nucleic acid sequences, i.e. PNC 1-605 or PNC
850-866 and PNC 894-906 or the encoded polypeptides; (4) an array
comprising two or more nucleic acids which bind to one or more nucleic
acid sequences, i.e. PNC 1-605 or PNC 850-866 and PNC 894-906; (5) a
method of treating or preventing PNC in a subject; (6) a composition, for
treating or preventing PNC, comprising a pharmaceutical amount of: (a) an
antisense polynucleotide or small interfering RNA against a
polynucleotide, i.e. PNC 1-259, PNC 606-640 and PNC 682-741 or PNC 850-
933; (b) an antibody or antibody fragment that binds to a protein encoded
by any one gene, i.e. PNC 1-259, PNC 606-640 and PNC 682-741 or PNC 850-
933; or (c) the compound obtained by the method of (2) as an active
ingredient and a pharmaceutical carrier; and (7) a method of predicting
recurrence of PNC. The compounds have cytostatic activity, and can be
used in vaccines and in gene therapy. The method is useful in diagnosing
PNC or a predisposition to developing PNC in a subject. The methods,
compounds and compositions are useful in treating or preventing PNC. The
polypeptides are useful as vaccines against PNC. The present sequence
represents a reverse transcription (RT) PCR primer used in semi-
quantitative RT-PCR experiments related to the diagnosis of PNC, which is
used in an example from the present invention.

Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

```
Query Match          63.0%; Score 12.6; DB 12; Length 20;
Best Local Similarity 78.9%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Qy 2 ACTCTTGCAGGAAGCGGCT 20
||| ||| ||| ||| ||| |||
Db 20 AATCTCCCAGGAAGCTGCT 2

Search completed: December 3, 2005, 13:29:58
Job time : 479 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:03:26 ; Search time 3651 Seconds
(without alignments)
256.297 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactctgcaggagcgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 52094

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsl1:*
10: gb_gsl2:*
11: gb_gsl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11.4	57.0	25	6	CB412589 ScaE_0880
2	11.4	57.0	28	6	CB412564 ScaE_0852
3	11	55.0	30	10	CZ477398 d10718-3p
C 4	10.8	54.0	30	2	BF209105 601872801
C 5	10.8	54.0	30	8	DN955287 it85c02.g
C 6	10.6	53.0	20	9	AZ314365 IM0031G07
C 7	10.6	53.0	24	11	TA273G07Q
C 8	10.6	53.0	26	9	AZ622081 IM0455E10
9	10.6	53.0	28	1	AA895705 vyl14d02.r
10	10.6	53.0	28	10	CL663977 PRI0145d
11	10.6	53.0	29	1	AL045592 DKFZp434N
12	10.6	53.0	30	1	AL045336 DKFZp434A
13	10.6	53.0	30	1	AL045352 DKFZp434B
14	10.6	53.0	30	1	AL045477 DKFZp434H
15	10.6	53.0	30	1	AL045487 DKFZp434I
C 16	10.4	52.0	18	1	AJ650912 AJ650912
17	10.4	52.0	23	11	TA278H12P
18	10.4	52.0	24	9	AZ468735
C 19	10.4	52.0	28	1	AI429345 mm95c09.x
C 20	10.4	52.0	29	9	AZ472735 IM0288G08
21	10.4	52.0	29	9	AZ771858 IM0574P16
22	10.4	52.0	29	9	BH849150 SALK_0693

C 23	10.4	52.0	29	10	CZ442916
24	10.4	52.0	30	3	BM400275
C 25	10.2	51.0	19	6	CD532073
C 26	10.2	51.0	20	9	AZ637794
27	10.2	51.0	22	1	AA915121
28	10.2	51.0	27	8	DL8733
29	10.2	51.0	27	10	CZ475704
C 30	10.2	51.0	29	9	BZ595262
31	10	50.0	27	9	AZ506426
32	10	50.0	29	10	CZ467258
33	10	50.0	29	11	TA36810P
34	10	50.0	30	10	CZ471369
35	9.8	49.0	22	1	AA912871
C 36	9.8	49.0	27	9	AZ660103
C 37	9.8	49.0	28	1	AA633771
38	9.8	49.0	28	1	AI005184
C 39	9.8	49.0	28	1	AA192663
C 40	9.8	49.0	29	10	AJ594066
41	9.8	49.0	30	10	CZ475056
C 42	9.8	49.0	30	11	TA285E07Q
C 43	9.6	48.0	20	9	AZ336487
C 44	9.6	48.0	23	11	TA201E03Q
45	9.6	48.0	25	8	L32049

ALIGNMENTS

RESULT 1
CB412589
LOCUS
DEFINITION
ScaE_0880 Bay scallop Uni-ZAP XR Expression Library Argopecten
irradians cDNA 5' similar to Argopecten irradians cDNA library,
unknown, mRNA sequence.
ACCESSION
CB412589
VERSION
CB412589.1 GI:56934150
KEYWORDS
EST.
SOURCE
Argopecten irradians
ORGANISM
Argopecten irradians
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
Pectinoidea; Pectinidae; Argopecten.
REFERENCE
1 (bases 1 to 25)
Song, L., Xu, W., Li, H., Wu, L., Xiang, J. and Guo, X.
The construction and EST analysis of cDNA library from bay scallop
Argopecten irradians
Unpublished (2003)
JOURNAL
COMMENT
Contact: Longtao Wu
Experimental Marine Biology Laboratory (EMBL)
Institute of Oceanology, Chinese Academy of Science (IOCAS)
7 Nanhai Road, Qingdao, Shandong 266071, P. R. China
Tel: +86-0532-2898552
Email: lshsong@ms.gdio.ac.cn
Seq primer: M13 Forward

FEATURES

source
1. .25
/organism="Argopecten irradians"
/mol_type="mRNA"
/db_xref="taxon:31199"
/sex="hermaphrodite"
/tissue_type="whole body"
/dev_stage="maturation phase"
/clone_lib="Bay scallop Uni-ZAP XR Expression Library"
/note="Organ: whole body; Vector: pBluescript (+/-);
Site 1: XhoI; Site 2: EcoRI; Using Stratagene's Uni-ZAP XR
cDNA synthesis kit, we constructed a cDNA library of Bay
scallop. 4975 ESTs were gained."

ORIGIN

Query Match 57.0%; Score 11.4; DB 6; Length 25;
Best Local Similarity 92.3%; Pred. No. 8.4e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 TGCAGGAGCGGC 19

```

||||| 8 TGCAGGAATCGGC 20

RESULT 2
CB412564 LOCUS
DEFINITION ScaE 0852 Bay scallop Uni-ZAP XR Expression Library Argopecten
            irradians cDNA 5' similar to Argopecten irradians cDNA library,
            unknown, mRNA sequence.
ACCESSION CB412564
VERSION    CB412564.1 GI:56934125
KEYWORDS   EST.
SOURCE     Argopecten irradians
ORGANISM   Argopecten irradians
            Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoidea;
            Pectinoidea; Pectinidae; Argopecten.
REFERENCE 1 (bases 1 to 28)
AUTHORS   Song,L., Xu,W., Li,H., Wu,L., Xiang,J. and Guo,X.
TITLE     The construction and EST analysis of cDNA library from bay scallop
            Argopecten irradians
JOURNAL   Unpublished (2003)
COMMENT   Contact: Longtao Wu
            Experimental Marine Biology Laboratory(EMBLCL)
            Institute of Oceanology, Chinese Academy of Science (IOCAS)
            7 Nanhai Road, Qingdao, Shandong 266071, P. R. China
            Tel: +86-0532-2898352
            Email: lshsong@ms.gdio.ac.cn
            Seq primer: M13 Forward.
            Location/Qualifiers
                1..28
                /organism="Argopecten irradians"
                /mol_type="mRNA"
                /db_xref="taxon:31199"
                /sex="hermaphrodite"
                /tissue_type="whole body"
                /dev_stage="maturation phase"
                /clone_lib="Bay scallop Uni-ZAP XR Expression Library"
                /note="Organ: whole body; Vector: pBluescript(+/-);
            Site_1: XhoI; Site_2: EcoRI; Using Stratagene's Uni-ZAP XR
            cDNA synthesis Kit, we constructed a cDNA library of Bay
            scallop. 4975 ESTs were gained."

ORIGIN
Query Match 57.0%; Score 11.4; DB 6; Length 28;
Best Local Similarity 92.3%; Pred. No. 8.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAATCGGC 19
Db 8 TGCAGGAATCGGC 20

RESULT 3
CZ477398 LOCUS
DEFINITION d10718-3prime Exelixis P element XP insertions Drosophila
            melanogaster genomic sequence recovered from 3' end of P element,
            genomic survey sequence.
ACCESSION CZ477398
VERSION    CZ477398.1 GI:62972730
KEYWORDS   GSS.
SOURCE     Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
            1 (bases 1 to 30)
REFERENCE 1
AUTHORS   Tibbault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
            Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
            Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
            Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Kilpack,K.,
            Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,

Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
Swimmer,C., Kopczyński,C., Doyk,G., Winberg,M.L. and Margolis,J.
A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
14981521
Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element.
The P element insertion position is 1 in the 30 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
    1..30
    /organism="Drosophila melanogaster"
    /mol_type="genomic DNA"
    /strain="isogenic w- strain"
    /db_xref="taxon:7227"
    /clone_lib="Exelixis P element XP insertions"
    /note="Vector: P element XP (GenBank accession number
    AY515149); An isogenic w- Drosophila melanogaster strain
    was mutagenized by remobilization of transposable
    elements. For the P element XP, we selected an easily
    mobilized ammunition element among inserts hopped onto the
    Binsyncy balancer. New insertions were collected in vias
    from dysgenic females using the standard chromosomal
    source of transposase, delta2-3. All lines were mapped to
    a chromosome by standard genetic methods, examined for
    homozygous viability and used for recovery of flanking
    genomic sequence by inverse PCR."

ORIGIN
Query Match 55.0%; Score 11; DB 10; Length 30;
Best Local Similarity 73.7%; Pred. NO. 1.4e+06;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGGAGCGGCT 20
Db 12 ACTCAGGAGGAAACCGCCT 30

RESULT 4
BF209105/c LOCUS
DEFINITION BF209105 30 bp mRNA linear EST 06-NOV-2000
            601872801F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4096776 5',
            mRNA sequence.
ACCESSION BF209105
VERSION    BF209105.1 GI:11102795
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
            1 (bases 1 to 30)
REFERENCE 1
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/;
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabs-x@mail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: CLONETECH Laboratories, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be

```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM961 row: a column: 01
High quality sequence stop: 30.

FEATURES
source

1..30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4096776"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_54"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgcttcggcc); Site 2: SfiI
(ggcattatggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
3' adaptor sequence:
5'-ATCTAGAGCGCGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

ORIGIN

Query Match 54.0%; Score 10.8; DB 2; Length 30;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTTGCAGGAAGCGG 18
Db 18 CTTGCAGGAAGCGG 5
||||| |

RESULT 5

DN955287/c
LOCUS
DEFINITION
it85c02.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.
ACCESSION
DN955287
VERSION
DN955287.1 GI:63027425
KEYWORDS
EST.
SOURCE
Gnetum gnemon
ORGANISM
Gnetum gnemon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales.
1 (bases 1 to 30)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)

Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.
Location/Qualifiers

FEATURES
source

1..30
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
/note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The

ORIGIN

Query Match 54.0%; Score 10.8; DB 8; Length 30;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 ACTCTTGACGGAAG 15
Db 14 ACCCTTGACGAGTAG 1
||||| |

RESULT 6

AZ314365/c
LOCUS
DEFINITION
AZ314365.1 GI:10360181
ACCESSION
AZ314365
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
SOURCE
ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 20)

REFERENCE
AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0031 row: G column: 07

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0031G07"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to

adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.0%; Score 10.6; DB 9; Length 20;
Best Local Similarity 76.5%; Pred. No. 2e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGCGGCT 20
||| ||||| ||| |||
Db 20 TCCTCCAGGAAGCAGGT 4

RESULT 7

TA273G07Q/c
LOCUS T. brucei sheared genomic DNA clone 273g07, linear GSS 13-DEC-2000
DEFINITION genomic survey sequence.

ACCESSION AL487649

VERSION AL487649.1 GI:11852459

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

REFERENCE Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 24)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsavedetior.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

Location/Qualifiers
1..24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="273g07"

ORIGIN

Query Match 53.0%; Score 10.6; DB 11; Length 24;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGCG 17
||| ||||| ||| |||

Db 18 GATCATTCAGGAAGCG 2

RESULT 8

AZ622081/c
LOCUS 1M0455E10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0455E10 R, genomic survey sequence.

ACCESSION AZ622081

VERSION AZ622081.1 GI:11744271

KEYWORDS GSS.

SOURCE

ORGANISM Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0455 row: E column: 10

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 26.

FEATURES

source

1..26
/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0455E10"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F."

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 53.0%; Score 10.6; DB 9; Length 26;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGCGGCT 20
||||| ||||| ||| |||

Db 24 TCTTGCAGTCAGCAGTT 8

RESULT 9

AA895705
LOCUS 28 bp mRNA linear EST 06-APR-1998
DEFINITION AA895705
clone IMAGE:1295427.5; similar to SW:DHAG_HUMAN P49189 ALDEHYDE
DEHYDROGENASE, E3 ISOZYME ;, mRNA sequence.

ACCESSION

AA895705

```

RA895705.1 GI:3032098
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurgomathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:676475
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 3.
Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1295427"
/tissue_type="macrophage"
/dev_stage="WEHI-3 cell_line"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse macrophage (#937306)"
/notes="Organ: blood; Vector: pBluescript SK-; Site 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt WEHI-3 cell line. Average insert size: 1.5 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGCAGG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Query Match 53.0%; Score 10.6; DB 1; Length 28;
Best Local Similarity 76.5%; Pred.No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAGCG 17
|||||
DB 11 GACACTTGTCTGGCAGTG 27
|||||

RESULT 10
LOCUS CL663977
DEFINITION CL663977.1 GI:50153867
Prionionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 28)
Srinivasan, J., Otto, G. W., Kahlow, U., Geisler, R. and Sommer, R. J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ

```

```
RESULT 12
AL045336          30 bp  mRNA  linear  EST 06-JUL-2004
LOCUS
DEFINITION      DKFPz434A095_r1 434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION      DKFPz434A095, mRNA sequence.
VERSION      AL045336
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 30)
AUTHORS      Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
              Wiemann,S.
TITLE      EST (Duesterhoeft, et al.)
JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
MIPS
FEATURES
source
    Location/Qualifiers
        1..30
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKFPz434A095"
        /tissue_type="testis"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="434 (synonym: htes3)"
        /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      53.0%; Score 10.6; DB 1; Length 30;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  ACTCTTCGAGGAGCGG 18
Db      5  ACGCCTGCAGGTACCGG 21

RESULT 13
AL045352          30 bp  mRNA  linear  EST 06-JUL-2004
LOCUS
DEFINITION      DKFPz434B075_r1 434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION      DKFPz434B075, mRNA sequence.
VERSION      AL045352
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 30)
AUTHORS      Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
              Wiemann,S.
TITLE      EST (Duesterhoeft, et al.)
JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
MIPS
FEATURES
source
    Location/Qualifiers
        1..30
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKFPz434B075"
        /tissue_type="testis"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="434 (synonym: htes3)"
        /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      53.0%; Score 10.6; DB 1; Length 30;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  ACTCTTCGAGGAGCGG 18
Db      5  ACGCCTGCAGGTACCGG 21

RESULT 14
AL045477          30 bp  mRNA  linear  EST 06-JUL-2004
LOCUS
DEFINITION      DKFPz434H225_r1 434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION      DKFPz434H225, mRNA sequence.
VERSION      AL045477
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 30)
AUTHORS      Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
              Wiemann,S.
TITLE      EST (Duesterhoeft, et al.)
JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
MIPS
FEATURES
source
    Location/Qualifiers
        1..30
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKFPz434H225"
        /tissue_type="testis"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="434 (synonym: htes3)"
        /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      53.0%; Score 10.6; DB 1; Length 30;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  ACTCTTCGAGGAGCGG 18
Db      5  ACGCCTGCAGGTACCGG 21

RESULT 15
AL045487          30 bp  mRNA  linear  EST 06-JUL-2004
LOCUS
DEFINITION      DKFPz434I105_r1 434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION      DKFPz434I105, mRNA sequence.
VERSION      AL045487
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 30)
AUTHORS      Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
              Wiemann,S.
TITLE      EST (Duesterhoeft, et al.)
JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
MIPS
FEATURES
source
    Location/Qualifiers
        1..30
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKFPz434I105"
        /tissue_type="testis"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="434 (synonym: htes3)"
        /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      53.0%; Score 10.6; DB 1; Length 30;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  ACTCTTCGAGGAGCGG 18
Db      5  ACGCCTGCAGGTACCGG 21
```

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/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      53.0%; Score 10.6; DB 1; Length 30;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  ACTCTTCGAGGAGCGG 18
Db      5  ACGCCTGCAGGTACCGG 21

RESULT 14
LOCUS
DEFINITION      DKFPz434H225_r1 434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION      DKFPz434H225, mRNA sequence.
VERSION      AL045477
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 30)
AUTHORS      Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
              Wiemann,S.
TITLE      EST (Duesterhoeft, et al.)
JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
MIPS
FEATURES
source
    Location/Qualifiers
        1..30
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKFPz434H225"
        /tissue_type="testis"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="434 (synonym: htes3)"
        /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      53.0%; Score 10.6; DB 1; Length 30;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  ACTCTTCGAGGAGCGG 18
Db      5  ACGCCTGCAGGTACCGG 21

RESULT 15
LOCUS
DEFINITION      DKFPz434I105_r1 434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION      DKFPz434I105, mRNA sequence.
VERSION      AL045487
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 30)
AUTHORS      Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
              Wiemann,S.
TITLE      EST (Duesterhoeft, et al.)
JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
MIPS
FEATURES
source
    Location/Qualifiers
        1..30
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKFPz434I105"
        /tissue_type="testis"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="434 (synonym: htes3)"
        /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match      53.0%; Score 10.6; DB 1; Length 30;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  ACTCTTCGAGGAGCGG 18
Db      5  ACGCCTGCAGGTACCGG 21
```

```

JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
             MIPS
FEATURES     Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
             Location/Qualifiers
             1..30
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="DKFZp434I105"
             /tissue_type="testis"
             /dev_stage="adult"
             /lab_host="DH10B"
             /clone_lib="434 (synonym: htes3)"
             /notes="Vector: pSPORT1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match          53.0%;   Score 10.6;   DB 1;   Length 30;
Best Local Similarity 76.5%;   Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2  ACTCTTTCGAGGAGCGG 18
        ||| ||||| |||
        5  ACCGCTGCAGGTACGG 21

Db

RESULT 16
LOCUS   AJ650912 CSQRAN19 Sus scrofa cDNA clone C0003276_L01, mRNA
DEFINITION
sequence.
ACCESSION   AJ650912
VERSION     AJ650912.1 GI:49327757
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.

REFERENCE   1 (bases 1 to 18)
            Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
            Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
            Unpublished (2004)
            Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross match with the -minscore 20
            and -mismatch 12 options. Vector:pBlueScriptII(KS) R. Site1: EcoRI
            R. Site2: NotI 5' Seq Primer M13p Normalised library constructed
            from pooled ovaries. Clones available from UK Centre for Functional
            Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
            EH25 9PS, www.ark-genomics.org.
            Location/Qualifiers
            1..18
            /organism="Sus scrofa"
            /mol_type="mRNA"
            /db_xref="taxon:9823"
            /clone="C0003276_L01"
            /tissue_type="ovary"
            /clone_lib="CSEQRAN19"
            /notes="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
            NotI; Single pass sequencing; Normalised library
            constructed from pooled ovaries"

ORIGIN
Query Match          52.0%;   Score 10.4;   DB 1;   Length 18;
Best Local Similarity 91.7%;   Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8  GCAGGAGGCGGC 19

```

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 JOURNAL plasmid inserts
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0281 row: I column: 14
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES

Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clones="UUGC1M0281114"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 [gil4732114]gb[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.0%; Score 10.4; DB 9; Length 24;
 Best Local Similarity 91.7%; Pred. No. 2.6e+06;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGG 12
 Db 7 GGCTCTTGCAGG 18

RESULT 19

AI429345/c
 LOCUS AI429345 28 bp mRNA linear EST 09-MAR-1999
 DEFINITION m95c09.x1 Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:551824 3', similar to TR:O15157 O15157 DOLICHOL MONOPHOSPHATE MANNOSE SYNTHASE 1, mRNA sequence.
 ACCESSION AI429345
 VERSION AI429345.1 GI:4275271
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 REFERENCE Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,

Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers
 1..28
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6 x CBA"
 /db_xref="taxon:10090"
 /clone="IMAGE:551824"
 /sex="female"
 /tissue_type="lung"
 /dev_stage="6-8 month old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse lung 937302"
 /notes="Organ: lung; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. 6-8 month old female lung and 1.5 year old male lung were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match 52.0%; Score 10.4; DB 1; Length 28;
 Best Local Similarity 91.7%; Pred. No. 2.6e+06;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CTTGCAGGAGC 16
 Db 28 CTTACAGGAGC 17

RESULT 20

AZ472735/c
 LOCUS AZ472735 29 bp DNA linear GSS 04-OCT-2000
 DEFINITION 1M0288G08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0288G08 F, genomic survey sequence.
 ACCESSION AZ472735
 VERSION AZ472735.1 GI:10630860
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
 1 (bases 1 to 29)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0288 row: G column: 08
 Seq primer: CGTTGTAACAGCGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES

Location/Qualifiers
 1. .29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0288G08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

source

1. .29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0574P16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.0%; Score 10.4; DB 9; Length 29;
 Best Local Similarity 91.7%; Pred. No. 2.6e+06;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAAGCGG 18
 |||||
 Db 21 TGCAGGAAGGGG 10

RESULT 21

AZ771858
 LOCUS
 DEFINITION 1M0574P16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0574P16 F, genomic survey sequence.

ACCESSION AZ771858
 VERSION AZ771858.1 GI:12894560

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 29)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0574 row: P column: 16

Seq primer: CGTTGTAACAGCGGCCAGT

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

source

1. .29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0574P16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.0%; Score 10.4; DB 9; Length 29;
 Best Local Similarity 70.0%; Pred. No. 2.6e+06;
 Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGCGGCT 20
 |||||
 Db 6 GACCTGCGAGGCGGCT 25

RESULT 22

BH849150

LOCUS

DEFINITION

BH849150 29 bp DNA linear GSS 13-JUN-2002
 SALK_069315.20.75.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_069315.20.75.x, genomic survey sequence.

ACCESSION BH849150

VERSION BH849150.1 GI:21420021

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 29)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salik.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within 300 bases of the 5' end of
 At2g40760.
 Class: TDNA tagged.

FEATURES

Location/Qualifiers
 1..29
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_069315.20.75.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 52.0%; Score 10.4; DB 9; Length 29;
 Best Local Similarity 70.0%; Pred. No. 2.6e+06;
 Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAGCGGCT 20
 ||||| ||||| ||||| |||||
 Db 8 GACTCGTACGGGAACACCT 27

RESULT 23

C2442916/c 29 bp DNA linear GSS 07-APR-2005
 LOCUS IBB3F03.fwd HIV-vector integration sites from well-expressed
 proviruses in human Jurkat T cells Homo sapiens genomic clone
 IBB3F03.fwd, genomic survey sequence.

C2442916.1 GI:62379009

GSS.

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

1 (bases 1 to 29)

Lewinski,M.K., Bisgrove,D., Shinn,P., Chen,H., Hoffmann,C.,

Hannenhalli,S., Verdin,E., Berry,C.C., Ecker,J.R. and Bushman,F.D.

Genome-wide analysis of chromosomal features repressing human

immunodeficiency virus transcription

J. Virol. 79 (11), 6610-6619 (2005)

15890899

Contact: Bushman FD

Department of Microbiology

University of Pennsylvania School of Medicine

402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA

19104-6076, USA

Tel: 215 573 8732

Fax: 215 573 4856

Email: bushman@mail.med.upenn.edu

Class: PCR with specific primers.

Location/Qualifiers

FEATURES

source
 1..29
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="IBB3F03.fwd"
 /call_line="Jurkat"
 /clone_lib="HIV-vector integration sites from
 well-expressed proviruses in human Jurkat T cells"
 /note="Vector: LTR-Tat-IRRES-GFP (pEV731); We have

investigated regulatory sequences in noncoding human DNA
 that are associated with repression of an integrated human
 immunodeficiency virus type 1 (HIV-1) promoter. HIV-1
 integration results in the formation of precise and
 homogeneous junctions between viral and host DNA, but
 integration takes place at many locations. Thus, the
 variation in HIV-1 gene expression at different
 integration sites reports the activity of regulatory
 sequences at nearby chromosomal positions. Negative
 regulation of HIV transcription is of particular interest
 because of its association with maintaining HIV in a
 latent state in cells from infected patients. To identify
 chromosomal regulators of HIV transcription, we infected
 Jurkat T cells with an HIV-based vector transducing green
 fluorescent protein (GFP) and separated cells into
 populations containing well-expressed (GFP-positive) or
 poorly expressed (GFP-negative) proviruses. We then
 determined the chromosomal locations of the two classes by
 sequencing 971 junctions between viral and cellular DNA.
 Possible effects of endogenous cellular transcription were
 characterized by transcriptional profiling. Low-level GFP
 expression correlated with integration in (i) gene
 deserts, (ii) centromeric heterochromatin, and (iii) very
 highly expressed cellular genes. These data provide a
 genome-wide picture of chromosomal features that repress
 transcription and suggest models for transcriptional
 latency in cells from HIV-infected patients."

ORIGIN

Query Match 52.0%; Score 10.4; DB 10; Length 29;
 Best Local Similarity 70.0%; Pred. No. 2.6e+06;
 Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAGCGGCT 20
 ||||| ||||| ||||| |||||
 Db 23 GTCTTTTCTCGGAGCTGCT 4

RESULT 24

BM400275

LOCUS

DEFINITION

BM400275 30 bp mRNA linear EST 17-JAN-2002

Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

Location/Qualifiers

source

1..30
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 52.0%; Score 10.4; DB 3; Length 30;
 Best Local Similarity 70.0%; Pred. No. 2.7e+06;
 Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGCGGCT 20
 ||||| | ||||| ||
 Db 8 GACTCACGGGGGCGAGCGCT 27

RESULT 25

CD532073/3
 LOCUS 13104 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA
 DEFINITION 3', mRNA sequence.

ACCESSION CD532073
 VERSION CD532073.1 GI:40452085
 KEYWORDS EST.

SOURCE

ORGANISM Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.

REFERENCE

1 (bases 1 to 19)
 Guo, Y., Cai, Z. and Gan, S.
 Transcription of Arabidopsis leaf senescence
 Plant Cell Environ. 27 (5), 521-549 (2004)

JOURNAL

COMMENT Contact: Susheng Gan
 Department of Horticulture
 Cornell University
 119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
 Tel: 607 254 5418
 Fax: 607 255 0599
 Email: sg288@cornell.edu
 Insert Length: 19 Std Error: 0.00
 Seq primer: 17
 POLYA=No.

FEATURES

source Location/Qualifiers
 1..19
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /ecotype="Landsberg erecta"
 /db_xref="taxon:3702"
 /tissue type="Leaf"
 /dev stage="Yellow Leaf With Greenish Base Area"
 /lab_host="E. coli"
 /clone_lib="Arabidopsis Leaf Senescence Library"
 /note="Organ: Rosette leaf; Vector: pBluescript SKII+;
 Site 1: ECORI; Site 2: EcoRI; Senescent rosette leaves #5
 and #6 (counted from the bottom) were harvested and
 immediately frozen in liquid N2. The leaves were visibly
 yellow excepted for the leaf base areas that were still
 greenish."

ORIGIN

Query Match 51.0%; Score 10.2; DB 6; Length 19;
 Best Local Similarity 80.0%; Pred. No. 3.1e+06;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTTGACGAGCGGC 19
 ||||| ||||| ||
 Db 19 CGTGAAGGAGCAGC 5

RESULT 26

AZ637794/3
 LOCUS 20 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0497D20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0497D20 F, genomic survey sequence.

ACCESSION AZ637794
 VERSION AZ637794.1 GI:11759984
 KEYWORDS GSS.

SOURCE

ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 20)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0497 row: D column: 20
 Seq primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0497D20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G114732114|9b|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0497D20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G114732114|9b|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 51.0%; Score 10.2; DB 9; Length 20;
 Best Local Similarity 80.0%; Pred. No. 3.2e+06;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGG 15
 ||||| ||||| ||
 Db 16 GGCTCTTGGAGGAG 2

RESULT 27

AA915121
 LOCUS 22 bp mRNA linear EST 14-APR-1998
 DEFINITION VZ03G03.r1 Soares mammary gland NbMMG Mus musculus cDNA clone
 IMAGE:1314676 5' similar to FR:Q15765 Q15765 VHL BINDING PROTEIN-1
 ;, mRNA sequence.
 ACCESSION AA915121

```

VERSION AA915121.1 GI:30545113
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Geisel, S., Kucaba, T., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Willson, R. and
Waterston, R.
TITLE The WashU-HWMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HWMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:684972
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m3 rev2 Et from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 22
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1314676"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_mammary_gland_NbMWG"
/notes="Organ: mammary gland; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1:
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGGCGCGCGAATGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

ORIGIN
Query Match 51.0%; Score 10.2; DB 1; Length 22;
Best Local Similarity 80.0%; Pred. No. 3.2e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAAG 15
| | | | | | | |
Db 8 GATTCCTTTCATGAAG 22

RESULT 28
D18733
DEFINITION MUSG01795 Mouse 3'-directed Mus musculus cDNA clone md0789 3',
mRNA sequence.
ACCESSION D18733
VERSION D18733.1 GI:1100702
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Kawanoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara, K.
TITLE Analysis of gene expression in mouse embryogenesis by 3'-directed
cDNA sequencing
JOURNAL Unpublished (1995)
COMMENT Contact: Shoko Kawamoto
Institute for Cellular and Molecular Biology
Osaka University
1-3, Yamadaoka, Suita, Osaka, 565, Japan
Email: shoko@next.imcb.osaka-u.ac.jp.
FEATURES
source
1. 27
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="md0789"
/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
/clone_lib="Mouse 3'-directed"

ORIGIN
Query Match 51.0%; Score 10.2; DB 8; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.3e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCTTGCGAGGAAGCGG 18
| | | | | | | |
Db 3 TCTTGCGAGTCAGCTG 17

RESULT 29
CZ475704
LOCUS 27 bp DNA linear GSS 29-APR-2005
DEFINITION d07387-Sprime Exelixis P element XP insertions Drosophila
melanogaster genomic Sequence recovered from 5' end of P element,
genomic survey sequence.
ACCESSION CZ475704 GI:62969731
VERSION CZ475704.1
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster

REFERENCE
AUTHORS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 27)
Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,
Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,
Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K.,
Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,
Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, P.,
Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
TITLE A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
JOURNAL Nat. Genet. 36 (3), 283-287 (2004)
PUBMED 14981521
COMMENT Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element.
The P element insertion position is 20 in the 27 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon insertion site.

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FEATURES
    source
        Location/Qualifiers
            1..27
                /organism="Drosophila melanogaster"
                /mol_type="genomic DNA"
                /strain="isogenic w- strain"
                /db_xref="taxon:7227"
                /clone_lib="Exelixis P element XP insertions"
                /note="Vector: P element XP (GenBank accession number AY515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized amminution element among inserts hopped onto the Binsincy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, Delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN
    Query Match      51.0%; Score 10.2; DB 10; Length 27;
    Best Local Similarity 80.0%; Pred. No. 3.3e+06;
    Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5 CTTGAGGAGGCGC 19
Db      13 CTCGAAGGAGGCG 27
        ||| ||||| |||
        ||| ||||| |||

RESULT 30
LOCUS   BZ595262/c      29 bp      DNA      linear      GSS 07-JAN-2003
DEFINITION
SALK_086377.15.90.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_086377.15.90.n, genomic
survey sequence.
ACCESSION   BZ595262
VERSION     BZ595262.1 GI:27535781
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 29)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
REFERENCE   A Sequence-Indexed Library of Insertion Mutations in the
AUTHORS     Arabidopsis Genome
            Unpublished (2001)
            Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At4g25580.
            Class: TDNA tagged.
            Location/Qualifiers
                1..29
                    /organism="Arabidopsis thaliana"
                    /mol_type="genomic DNA"
                    /ecotype="Col-0"
                    /db_xref="taxon:3702"
                    /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                    /note="PCR was performed on Arabidopsis thaliana lines
                    each of which contains one or more TDNA insertion
                    elements. The resultant fragment for each line was
                    directly sequenced to determine the genomic sequence at
                    the site of insertion. Details of the protocols used can
                    be found at http://signal.salk.edu/tdna_protocols.html"

FEATURES
    source
        Location/Qualifiers
            1..27
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UGGCM0347M04"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UGGCM1 library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into

```

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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ORIGIN
Query Match          50.0%; Score 10; DB 9; Length 27;
Best Local Similarity 72.2%; Pred. No. 4.1e+06;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACTCTTGCGAGGACGG 18
    |||||
Db 5 GCCTGTTGTAGGAGGGG 22

RESULT 32
CZ467258          29 bp DNA linear GSS 29-APR-2005
LOCUS
DEFINITION
col566-5prime Exelixis piggyBac PB insertions Drosophila
melanogaster genomic sequence recovered from 5' end of piggyBac,
genomic survey sequence.
CZ467258
CZ467258.1 GI:62961271
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 29)
REFERENCE
AUTHORS
Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
Laifer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
Swimmer,C., Kopczyński,C., Duyk,G., Winberg,M.L. and Margolis,J.
A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
14981521
COMMENT
Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: Rhoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
piggyBac element.
The piggyBac insertion position is 26 in the 29 bases. This
insertion position refers to the first base of the 4 base TTAA
target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
1. .29
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac PB insertions"
/notes="Vector: piggyBac PB (GenBank accession number
AY515146); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the PB element using
Hsp70:piggyBac transposase from a single ammunition
element on either the X or third chromosome. We induced
transposase expression by immersing bottles in a
circulating 370C water bath for a daily (days 3-10 after
egg-laying) 1-h heat shock. We outcrossed the resulting
dysgenic males to an isogenic w- strain. New insertions
were identified on the basis of a change in eye color
(third chromosome ammunition) or the appearance of w+ male
progeny (X chromosome ammunition). All lines were mapped

```

to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

```

ORIGIN
Query Match          50.0%; Score 10; DB 10; Length 29;
Best Local Similarity 72.2%; Pred. No. 4.2e+06;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CTCTTGCGAGGACGGCT 20
    |||||
Db 5 CTCTGGAACGGCGCGCT 22

RESULT 33
TA36B10P          29 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 36b10, forward sequence,
genomic survey sequence.
AL453638
AL453638.1 GI:11854781
GSS.
Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 29)
REFERENCE
AUTHORS
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.B., Rajandream,M.A. and Barrell,B.G.
Direct Submision
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1. .29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="36b10"

FEATURES
source
1. .29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="36b10"

ORIGIN
Query Match          50.0%; Score 10; DB 11; Length 29;
Best Local Similarity 72.2%; Pred. No. 4.2e+06;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CTCTTGCGAGGACGGCT 20
    |||||
Db 9 CTGCTGTCGAGGCGGAT 26

RESULT 34
CZ471369          30 bp DNA linear GSS 29-APR-2005
LOCUS
DEFINITION
d00081-3prime Exelixis P element XP insertions Drosophila
melanogaster genomic sequence recovered from 3' end of P element,
genomic survey sequence.
CZ471369
CZ471369.1 GI:62965382

```


Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0538 row: B column: 01
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers

FEATURES

1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0538B01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

* ORIGIN

Query Match 49.0%; Score 9.8; DB 9; Length 27;
 Best Local Similarity 84.6%; Pred. No. 5.2e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGGC 19
 |||||
 Db 19 TGCAGGAATTGCC 7

RESULT 37
 AA633771/c
 LOCUS
 DEFINITION
 ac27e01.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:857688 3' similar to SW:CYB_HUMAN P00156 CYTOCHROME B ;, mRNA sequence.

ACCESSION
 VERSION
 AA633771.1 GI:2556985
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM

REFERENCE
 AUTHORS
 Hillier, L., Allen, M., Bowles, J., Dubuque, T., Geisler, G., Jost, S., Krizman, D., Kucaba, F., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE
 JOURNAL
 COMMENT
 WashU-NCI human EST Project
 Unpublished (1997)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Insert Length: 709 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

1..28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:857688"
 /sex="female"
 /dev_stage="49 year old"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Stratagene ovary (#937217)"
 /notes="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Total ovary tissue, normal, caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGCAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
 Best Local Similarity 84.6%; Pred. No. 5.2e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGGC 19
 |||||
 Db 15 TGTAGGAAGAGGC 3

RESULT 38
 AI005184
 LOCUS
 DEFINITION

ou60501.x1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1632169 3' similar to TR:Q13162 Q13162 ANTIOXIDANT ENZYME AOE37-2. ;, mRNA sequence.

ACCESSION
 VERSION
 AI005184.1 GI:3214694
 EST.
 KEYWORDS
 SOURCE
 Homo sapiens (human)
 ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 28)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio-llnl.gov/bbrp/image/image.html

Insert Length: 1005 Std Error: 0.00

Seq primer: primer name ambiguous

High quality sequence stop: 1.

FEATURES

1..28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1632169"

/sex="female, pooled"
 /tissue_type="breast"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Br2"
 /note="Vector: PTT3D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from pooled bulk
 breast tumor tissue, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pTT3
 vector. This library is the normalized version of
 NCI CGAP Br1.1. Library was constructed by Bento Soares
 and M. Fatima Bonaldo."

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
 Best Local Similarity 84.6%; Pred. No. 5.2e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 6 TTGCAGGAAGCGG 18
 Db 1 TTGAAAGAGCGG 13

RESULT 39

AA192663/c
 LOCUS
 DEFINITION 28 bp mRNA linear EST 12-MAR-1998
 zq03f12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone
 IMAGE:628655 3' similar to TR:G556044 G556044 CYTOCHROME B ;, mRNA
 sequence.

ACCESSION

VERSION
 KEYWORDS
 SOURCE

ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

1 (bases 1 to 28)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
 Martin, J., Moore, B., Schellenberg, K., Steproe, N., Tan, F.,
 Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
 WASHU-NCI human EST Project
 Unpublished (1997)

TITLE

JOURNAL
 COMMENT
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available royalty-free through LILN; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Insert Length: 825 Std Error: 0.00
 Seq primer: -40M13 fwd. from AmerSham
 High quality sequence stop: 1.

FEATURES

source

1..28
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:5048889"
 /db_xref="taxon:9606"
 /clone="IMAGE:628655"
 /tissue_type="muscle"
 /dev_stage="adult"

/lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene muscle 937209"
 /note="Organ: skeletal muscle; Vector: pBluescript SK-;
 Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally.
 Primer: Oligo dT. Skeletal muscle from patient with
 malignant hyperthermia. Average insert size: 1.0 Kb;

Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGAG
 3' -3' adaptor sequence: 5' CTCAGTGTGTGTGTGTGTGTGT 3'

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
 Best Local Similarity 84.6%; Pred. No. 5.2e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 7 TGCAGGAAGCGGC 19
 Db 15 TGTAGGAAGAGCG 3

RESULT 40

AJ594066/c
 LOCUS
 DEFINITION 29 bp DNA linear GSS 15-JAN-2004
 Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 392C12, genomic survey sequence.

ACCESSION

VERSION
 KEYWORDS
 SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

1
 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelleter, G.,
 Lepiniec, L., Caboche, M. and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites

TITLE

JOURNAL
 PUBMED
 REFERENCE

AUTHORS

12446565
 2 (bases 1 to 29)
 Balzergue, S.
 Direct Submission
 Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
 http://dbgap-versailles.inra.fr/publiclines/. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplatte' (http://www.genoplatte.com and
 http://genoplatte-info.infobiogen.fr).

FEATURES

source

1..29
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="392C12"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Wassilewskija"
 misc_feature 1..29
 /note="T-DNA flanking sequence
 left border"

ORIGIN

Query Match 49.0%; Score 9.8; DB 10; Length 29;
 Best Local Similarity 84.6%; Pred. No. 5.2e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 ACTCTTCAGGAA 14
 Db 28 AATCTTCAGGAA 16

Search completed: December 3, 2005, 15:07:09

Job time : 3655 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:17:55 ; Search time 137 Seconds
(without alignments)
259.498 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactcttcgaggaagcggt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1026780

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_NA.*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
7: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14.8	74.0	25	3	US-09-396-196G-124305
C 2	14.2	71.0	25	3	US-09-396-196G-65325
C 3	14	70.0	20	3	US-09-288-461-19
C 4	14	70.0	20	3	US-09-758-881-19
C 5	13.8	69.0	28	3	US-08-137-134B-13
C 6	13.6	68.0	25	3	US-09-396-196G-3439
C 7	13.6	68.0	25	3	US-09-396-196G-42438
C 8	13.2	66.0	23	3	US-09-496-444-6
C 9	13.2	66.0	25	3	US-09-396-196G-40794
C 10	13.2	66.0	25	3	US-09-396-196G-65314
C 11	13.2	66.0	25	3	US-09-396-196G-88577
C 12	13.2	66.0	25	3	US-09-396-196G-88578
C 13	12.8	64.0	20	3	US-09-081-385-134
C 14	12.8	64.0	20	3	US-09-752-639-134
C 15	12.8	64.0	20	3	US-09-712-813-134
C 16	12.8	64.0	20	3	US-09-700-354A-134
C 17	12.8	64.0	25	3	US-09-396-196G-26683
C 18	12.8	64.0	25	3	US-09-396-196G-26684
C 19	12.8	64.0	25	3	US-09-396-196G-26685
C 20	12.8	64.0	25	3	US-09-396-196G-107676
C 21	12.8	64.0	25	3	US-09-396-196G-107677
C 22	12.8	64.0	25	3	US-09-396-196G-107678
C 23	12.8	64.0	25	3	US-09-396-196G-107679
C 24	12.8	64.0	25	3	US-09-396-196G-108203

Sequence 30, Appl
Sequence 7, Appl
Sequence 86, Appl
Sequence 86, Appl
Sequence 86, Appl
Sequence 13006, A
Sequence 13007, A
Sequence 13008, A
Sequence 13009, A
Sequence 13010, A
Sequence 13011, A
Sequence 13012, A
Sequence 56156, A
Sequence 8, Appl
Sequence 77, Appl
Sequence 79, Appl
Sequence 79, Appl
Sequence 79, Appl
Sequence 79, Appl
Sequence 79, Appl

25 12.6 63.0 21 3 US-09-972-115A-30
26 12.6 63.0 22 2 US-08-749-852-7
27 12.6 63.0 23 2 US-08-297-299B-86
28 12.6 63.0 23 2 US-08-858-083-86
29 12.6 63.0 23 6 PCT-US95-11029-86
30 12.6 63.0 25 3 US-09-866-108A-13006
31 12.6 63.0 25 3 US-09-866-108A-13007
32 12.6 63.0 25 3 US-09-866-108A-13008
33 12.6 63.0 25 3 US-09-866-108A-13009
34 12.6 63.0 25 3 US-09-866-108A-13010
35 12.6 63.0 25 3 US-09-866-108A-13011
36 12.6 63.0 25 3 US-09-866-108A-13012
37 12.6 63.0 25 3 US-09-396-196G-56156
38 12.6 63.0 30 3 US-09-449-335-8
39 12.4 62.0 20 2 US-08-171-718-77
40 12.4 62.0 20 3 US-08-478-087-77
41 12.4 62.0 20 3 US-09-135-020-79
42 12.4 62.0 20 3 US-09-135-010A-79
43 12.4 62.0 20 3 US-09-444-871-79
44 12.4 62.0 20 3 US-09-597-735-79
45 12.4 62.0 20 3 US-09-444-295-79

ALIGNMENTS

RESULT 1
US-09-396-196G-124305/c
; Sequence 124305, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124305
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-124305

Query Match 74.0%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACTCTTCGAGGACCG 18
DB 19 GGCTCTTCGAGGACGAG 2

RESULT 2
US-09-396-196G-65325
; Sequence 65325, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65325
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65325

Query Match 71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGGAAGCGGCT 20
||||| ||| ||| |||
Db 5 ACTCTTCAGGAAGTGGCT 23

RESULT 3
US-09-288-461-19
; Sequence 19, Application US/09288461
; Patent No. 6159694
; GENERAL INFORMATION:
; APPLICANT: Karrias, James G.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0338
; CURRENT APPLICATION NUMBER: US/09/288,461
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-288-461-19

Query Match 70.0%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAA 14
||||| ||| ||| |||
Db 7 GACTCTTGCAGGAA 20

RESULT 4
US-09-758-881-19
; Sequence 19, Application US/09758881
; Patent No. 6727064
; GENERAL INFORMATION:
; APPLICANT: Karrias, James G.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0532
; CURRENT APPLICATION NUMBER: US/09/758,881
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-881-19

Query Match 70.0%; Score 14; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAA 14
||||| ||| ||| |||
Db 7 GACTCTTGCAGGAA 20

RESULT 5
US-08-137-134B-13
; Sequence 13, Application US/08137134B
; Patent No. 6369038
; GENERAL INFORMATION:
; APPLICANT: BLUMENFELD, Marta
; APPLICANT: BRANDYS, Pascal
; APPLICANT: D'AURIOL, Luc
; APPLICANT: VASSEUR, Marc
; TITLE OF INVENTION: CLOSED SENSE AND ANTISENSE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN
; STREET: 400 Seventh Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,134B
; FILING DATE: 23-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/05114
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PLAYER, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P58359
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-137-134B-13

Query Match 69.0%; Score 13.8; DB 3; Length 28;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CTCTTCAGGAAGCGGC 19
||||| ||| ||| ||| |||
Db 12 CTCTTCAGGAAGCGGC 28

RESULT 6
US-09-396-196G-3439/c
; Sequence 3439, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; EARLIER FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3439
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-3439

Query Match 68.0%; Score 13.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGCGGCT 20
||| ||||| ||||| |||||
Db 21 GAACCTTCAGGAGCGTGT 2

RESULT 7
US-09-396-196G-42438
; Sequence 42438, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-42438

Query Match 68.0%; Score 13.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGCGGCT 20
||| ||||| ||||| |||||
Db 4 GACTCTTCGGGTAGTCT 23

RESULT 8
US-09-496-444-6/c
; Sequence 6, Application US/09496444
; Patent No. 6933376
; GENERAL INFORMATION:
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm William J.
; APPLICANT: Lowe, Keith S.
; APPLICANT: Bailey, Matthew A.
; TITLE OF INVENTION: Cell Cycle Polynucleotide, Polypeptide,
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 1109
; CURRENT APPLICATION NUMBER: US/09/496,444
; CURRENT FILING DATE: 2000-02-02
; EARLIER APPLICATION NUMBER: US 60/119,857
; EARLIER FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: US 60/101,551

; EARLIER FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: US 09/398,858
; EARLIER FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: US 09/257,131
; EARLIER FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)...(23)
US-09-496-444-6

Query Match 66.0%; Score 13.2; DB 3; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCTTGCAGGAAGCGGCT 20
||| ||||| ||||| |||||
Db 19 CTGTTGCAGCAAGCGGT 2

RESULT 9
US-09-396-196G-40794/c
; Sequence 40794, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40794
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-40794

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCTTGCAGGAAGCGGCT 20
||| ||||| ||||| |||||
Db 20 CTATGGCTGGAAGCGGT 3

RESULT 10
US-09-396-196G-65314
; Sequence 65314, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65314
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65314

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGGAAGCGGC 19
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8 ACTCTTCAGGAAGTGGC 25

RESULT 11
US-09-396-196G-88577
; Sequence 88577, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88577
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88577

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGGAAGCGGC 19
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5 AGTCTTCAGGAGCAGC 22

RESULT 12
US-09-396-196G-88578
; Sequence 88578, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88578
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88578

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 ACTCTTCAGGAAGCGGC 19
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 AGTCTTCAGGAGCAGC 19

RESULT 13
US-09-081-385-134
; Sequence 134, Application US/09081385
; Patent No. 6593456
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,385
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-081-385-134

Query Match 64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGC 19
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 TCTTCCAGGAAGTGTC 16

RESULT 14
US-09-752-639-134
; Sequence 134, Application US/09752639
; Patent No. 6911314
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods

;; TITLE OF INVENTION: of Use Thereof
;; NUMBER OF SEQUENCES: 154
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 755 PAGE MILL ROAD
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows
;; SOFTWARE: FastSEQ for Windows Version 2.0b
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/752,639
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US99/10793
;; FILING DATE:
;; APPLICATION NUMBER: 09/081,385
;; FILING DATE:
;; APPLICATION NUMBER: 08/964,747
;; FILING DATE: 05-NOV-1997
;; APPLICATION NUMBER: 60/030,761
;; FILING DATE: 06-NOV-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wu, Frank
;; REGISTRATION NUMBER: 41,386
;; REFERENCE/DOCKET NUMBER: 22000-20577.21
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-813-5600
;; TELEFAX: 650-494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 134:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; NAME: Wu, Frank
;; REGISTRATION NUMBER: 41,386
;; REFERENCE/DOCKET NUMBER: 22000-20577.21
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-813-5600
;; TELEFAX: 650-494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 134:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-09-752-639-134

Query Match 64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTCAGGAGCGGC 19
Db 1 TCTTCAGGAGCGTC 16

RESULT 15
US-09-712-813-134
; Sequence 134, Application US/09712813
; Patent No. 6930084
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; Factor Receptor Releasing Enzyme Activity, and Methods
; of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: Windows
;; SOFTWARE: FastSEQ for Windows Version 2.0b
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/712,813
;; FILING DATE: 13-NOV-1997
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/081,385
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: 08/964,747
;; FILING DATE: 05-NOV-1997
;; APPLICATION NUMBER: 60/030,761
;; FILING DATE: 06-NOV-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wu, Frank
;; REGISTRATION NUMBER: 41,386
;; REFERENCE/DOCKET NUMBER: 22000-20577.21
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-813-5600
;; TELEFAX: 650-494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 134:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; NAME: Wu, Frank
;; REGISTRATION NUMBER: 41,386
;; REFERENCE/DOCKET NUMBER: 22000-20577.21
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-813-5600
;; TELEFAX: 650-494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 134:
;; SEQUENCE DESCRIPTION: SEQ ID NO: 134:
;; US-09-712-813-134

Query Match 64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTCAGGAGCGGC 19
Db 1 TCTTCAGGAGCGTC 16

RESULT 16
US-09-700-354A-134
; Sequence 134, Application US/09700354A
; Patent No. 6955894
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, Tetsuya
; Granger, Gale A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; Factor Receptor Releasing Enzyme Activity.
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BOZICEVIC, FIELD, & FRANCIS, LLP
; STREET: 200 MIDDLEFIELD ROAD, #200
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/700,354A
; FILING DATE: 17-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/081,385
; FILING DATE: 14-MAY-1998
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE: 14-MAY-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Francis, Carol L.
; REGISTRATION NUMBER: 36,513

```
; REFERENCE/DOCKET NUMBER: IRVN-007CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650-327-3231
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-09-700-354A-134

Query Match          64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 TCTTGCAGGAAGCGGC 19
Db      1 TCTTCCAGGAAGCTGC 16

RESULT 17
US-09-396-196G-26683/c
; Sequence 26683, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26683
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-26683

Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 TCTTGCAGGAAGCGGC 19
Db      25 TCGTCCAGGAAGCGGC 10

RESULT 18
US-09-396-196G-26684/c
; Sequence 26684, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26684
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-26684

Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 TCTTGCAGGAAGCGGC 19
Db      22 TCGTCCAGGAAGCGGC 7

RESULT 19
US-09-396-196G-26685/c
; Sequence 26685, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26685
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-26685

Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 TCTTGCAGGAAGCGGC 19
Db      16 TCGTCCAGGAAGCGGC 1

RESULT 20
US-09-396-196G-107676/c
; Sequence 107676, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107676
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-107676

Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```


Qy 1 GACTCTTGCAGGAAGC 16
|||||
Db 25 GACTCTTGCATGATGC 10

RESULT 21
US-09-396-196G-107677/c
; Sequence 107677, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107677
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107677

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAGC 16
|||||
Db 23 GACTCTTGCATGATGC 8

RESULT 22
US-09-396-196G-107678/c
; Sequence 107678, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107678
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107678

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAGC 16
|||||
Db 22 GACTCTTGCATGATGC 7

RESULT 23
US-09-396-196G-107679/c
; Sequence 107679, Application US/09396196G
; Patent No. 6821724

; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107679
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107679

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAGC 16
|||||
Db 16 GACTCTTGCATGATGC 1

RESULT 24
US-09-396-196G-108203/c
; Sequence 108203, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-108203

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTTGCAGGAAGCGGCT 20
|||||
Db 17 CTTGAATGAGCGGCT 2

RESULT 25
US-09-972-115A-30
; Sequence 30, Application US/09972115A
; Patent No. 659728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05

;; PRIOR APPLICATION NUMBER: US 60/128,577
;; PRIOR FILING DATE: 2000-04-10
;; PRIOR APPLICATION NUMBER: US 60/129,123
;; PRIOR FILING DATE: 1999-04-13
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 30
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Primer
US-09-972-115A-30

Query Match 63.0%; Score 12.6; DB 3; Length 21;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAGCGGC 19
||| |||| |||| |||| ||
Db 3 GACAATTGCTGGAAGCTGC 21

RESULT 26
US-08-749-852-7
; Sequence 7, Application US/08749852
; Patent No. 5874222
; GENERAL INFORMATION:
; APPLICANT: JIRTLE, RANDY L.
; APPLICANT: DE SOUZA, ANGUS T.
; APPLICANT: HANKINS, GERALD R.
; TITLE OF INVENTION: TUMOR SUPPRESSOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P. C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,852
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-749-852-7

Query Match 63.0%; Score 12.6; DB 2; Length 22;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAGCGGC 19
||| |||| |||| |||| ||
Db 4 GACTGTTCTGGAAGCAGC 22

RESULT 27
US-08-297-299B-86
; Sequence 86, Application US/08297299B
; Patent No. 5656427
; GENERAL INFORMATION:
; APPLICANT: Phillip Hammond and
; APPLICANT: Anthony Endozo
; TITLE OF INVENTION: NUCLEIC ACID HYBRIDI-
; TITLE OF INVENTION: ZATION ASSAY PROBES,
; TITLE OF INVENTION: HELPER PROBES AND
; TITLE OF INVENTION: AMPLIFICATION OLIGO-
; TITLE OF INVENTION: NUCLEOTIDES TARGETED TO
; TITLE OF INVENTION: MYCOPLASMA PNEUMONIAE
; TITLE OF INVENTION: NUCLEIC ACID
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,299B
; FILING DATE: August 29, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: n/a
; FILING DATE: n/a
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 208/130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-297-299B-86

Query Match 63.0%; Score 12.6; DB 2; Length 23;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAGCGGC 19
||| |||| |||| |||| ||
Db 5 GACTTACGAGCAATGCGC 23

RESULT 28
US-08-858-083-86
; Sequence 86, Application US/08858083
; Patent No. 5969122
; GENERAL INFORMATION:
; APPLICANT: Phillip Hammond and
; APPLICANT: Anthony Endozo
; TITLE OF INVENTION: NUCLEIC ACID HYBRIDI-
; TITLE OF INVENTION: ZATION ASSAY PROBES,
US-08-858-083-86

TITLE OF INVENTION: HELPER PROBES AND
TITLE OF INVENTION: AMPLIFICATION OLIGO-
TITLE OF INVENTION: NUCLEOTIDES TARGETED TO
TITLE OF INVENTION: MYOGLIPLASMA PNEUMONIAE
TITLE OF INVENTION: NUCLEIC ACID
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/858,083

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/297,299

FILING DATE: August 29, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Heber, Sheldon O.

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 208/130

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 86:

SEQUENCE CHARACTERISTICS:

LENGTH: 23

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-858-083-86

Query Match 63.0%; Score 12.6; DB 2; Length 23;

Best Local Similarity 78.9%; Pred. No. 4.5e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GACTCTTCGAGGACGCGC 19

Db 5 GACTCTAGCAGCAATGCGC 23

RESULT 29

PCT-US95-11029-86

Sequence 86, Application PC/TUS9511029

GENERAL INFORMATION:

APPLICANT: GEN-PROBE INCORPORATED

TITLE OF INVENTION: NUCLEIC ACID HYBRIDIZATION

TITLE OF INVENTION: ASSAY PROBES, HELPER PROBES

TITLE OF INVENTION: AND AMPLIFICATION OLIGO-

TITLE OF INVENTION: NUCLEOTIDES TARGETED

TITLE OF INVENTION: TO MYOGLIPLASMA PNEUMONIAE

TITLE OF INVENTION: NUCLEIC ACID

NUMBER OF SEQUENCES: 92

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: California

ZIP: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS (Version 6.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11029
FILING DATE:
PRIOR APPLICATION DATA: Prior applications total
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: One
APPLICATION NUMBER: 08/297,299
FILING DATE: 29 August 1994
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 208/130-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-11029-86

Query Match 63.0%; Score 12.6; DB 6; Length 23;

Best Local Similarity 78.9%; Pred. No. 4.5e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GACTCTTCGAGGACGCGC 19

Db 5 GACTCTAGCAGCAATGCGC 23

RESULT 30

US-09-866-108A-13006

Sequence 13006, Application US/09866108A

Patent No. 6686188

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: PENN, Sharron G.

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: ABOICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

```
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13006
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13006

Query Match      63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGACGAGACGGCT 20
Db 7 AGTCCTGCCAGACGGCT 25

RESULT 31
US-09-866-108A-13007
; Sequence 13007, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13007
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13007

Query Match      63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGACGAGACGGCT 20
Db 6 AGTCCTGCCAGACGGCT 24

RESULT 32
US-09-866-108A-13008
; Sequence 13008, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13008
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13008

Query Match      63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGACGAGACGGCT 20
Db 5 AGTCCTGCCAGACGGCT 23

RESULT 33
US-09-866-108A-13009
; Sequence 13009, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
```

; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13009
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13009

Query Match 63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGCGAGGCGGCT 20
Db 4 AGTCTGCCAGAGCGGCT 22

RESULT 34
US-09-866-108A-13010
; Sequence 13010, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13010
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13010

Query Match 63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGCGAGGCGGCT 20
Db 3 AGTCTGCCAGAGCGGCT 21

RESULT 35
US-09-866-108A-13011
; Sequence 13011, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13011
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13011

Query Match 63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGCGAGGCGGCT 20
Db 3 AGTCTGCCAGAGCGGCT 21

```
Db      2 AGTCTGCCAGAGCGGCT 20

RESULT 36
US-09-866-108A-13012
; Sequence 13012, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13012
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-866-108A-13012

Query Match      63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db      1 AGTCTGCCAGAGCGGCT 19

RESULT 37
US-09-396-196G-56156
; Sequence 56156, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56156
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-56156

Query Match      63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 ACTCTTGCGAGGAGCGGCT 20
        ||||| ||||| ||||| |||||
Db      7 ACTCTTACGAAAGCGGCT 25

RESULT 38
US-09-449-335-8
; Sequence 8, Application US/09449335
; Patent No. 6303365
; GENERAL INFORMATION:
; APPLICANT: Busch, Marco
; APPLICANT: Hain, Rudiger
; APPLICANT: Martin, William
; APPLICANT: Tietjen, Klaus
; APPLICANT: Kloti, Andreas
; TITLE OF INVENTION: Method of determining the activity of
; TITLE OF INVENTION: 1-deoxy-D-xylulose-5-phosphate reductoisomerase and
; FILE REFERENCE: 2020US
; CURRENT APPLICATION NUMBER: US/09/449,335
; CURRENT FILING DATE: 1999-11-24
; EARLIER APPLICATION NUMBER: DE 199 35 967.9
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-449-335-8

Query Match      63.0%; Score 12.6; DB 3; Length 30;
Best Local Similarity 78.9%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GACTCTTGCGAGGAGCGGC 19
        ||||| ||||| ||||| |||||
Db      8 GACTCATGATGAAGTGGC 26

RESULT 39
US-08-171-718-77/c
; Sequence 77, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,718
FILING DATE: 22-DEC-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,034
FILING DATE: 25-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REFERENCE/DOCKET NUMBER: 0609.3850003
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-171-718-77

Query Match 62.0%; Score 12.4; DB 2; Length 20;
Best Local Similarity 92.9%; Pred. No. 5.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CTCTTGCGAGGAGC 16
||| ||||| |||
Db 15 CTCTTGCGAGGTAGC 2

RESULT 40
US-08-478-087-77/G
Sequence 77, Application US/08478087
Patent No. 6077685
GENERAL INFORMATION:
APPLICANT: Trofatter, James A.
APPLICANT: MacCollin, Mia M.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,087
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,718
FILING DATE: 22-DEC-1993
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,034

FILING DATE: 25-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REFERENCE/DOCKET NUMBER: 0609.3850003
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-087-77

Query Match 62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 5.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CTCTTGCGAGGAGC 16
||| ||||| |||
Db 15 CTCTTGCGAGGTAGC 2

Search completed: December 3, 2005, 15:09:35
Job time : 138 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:22:14 ; Search time .796 Seconds
(without alignments)
207.773 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactcttgacgagcgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 10535742

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_Main:*
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	9	US-10-773-678-342
2	20	100.0	29	9	US-10-773-678-158
3	19	95.0	20	9	US-10-773-678-179
4	19	95.0	20	9	US-10-773-678-341
5	18	90.0	20	9	US-10-773-678-340
6	17	85.0	20	9	US-10-773-678-343
7	17	85.0	20	9	US-10-773-678-344
8	16.4	82.0	25	9	US-10-956-157-186717
9	16	80.0	20	9	US-10-857-715-201
10	15.2	76.0	25	9	US-10-956-157-301412
11	15.2	76.0	25	10	US-11-060-756-287536
12	15	75.0	20	9	US-10-773-678-339
13	15	75.0	20	9	US-10-773-678-345
14	14.8	74.0	25	7	US-10-719-956-135575
15	14.8	74.0	25	7	US-10-719-956-196148
16	14.8	74.0	25	8	US-10-719-900-191405
17	14.8	74.0	25	9	US-10-809-189-124305
18	14.8	74.0	25	9	US-10-956-157-205933
19	14.4	72.0	25	8	US-10-719-900-611442
20	14.4	72.0	25	9	US-10-956-157-178444
21	14.4	72.0	25	10	US-11-036-317-95537
22	14.2	71.0	21	8	US-10-751-736-54782
23	14.2	71.0	25	7	US-10-719-956-51664

24	14.2	71.0	25	9	US-10-809-189-65325	Sequence 65325, A
25	14.2	71.0	25	10	US-11-036-317-193968	Sequence 193968, A
26	14.2	71.0	25	10	US-11-036-317-247028	Sequence 247028, A
27	14.2	71.0	25	10	US-11-036-317-255809	Sequence 255809, A
28	14.2	71.0	25	10	US-11-036-317-289853	Sequence 289853, A
29	14.2	71.0	25	10	US-11-036-317-308860	Sequence 308860, A
30	14.2	71.0	25	10	US-11-036-317-435916	Sequence 435916, A
31	14.2	71.0	25	10	US-11-036-317-473142	Sequence 473142, A
32	14.2	71.0	25	10	US-11-036-317-482672	Sequence 482672, A
33	14.2	71.0	25	10	US-11-036-317-538007	Sequence 538007, A
34	14.2	71.0	25	10	US-11-036-317-634153	Sequence 634153, A
35	14.2	71.0	25	10	US-11-036-317-648448	Sequence 648448, A
36	14.2	71.0	25	10	US-11-036-317-773627	Sequence 773627, A
37	14.2	71.0	25	10	US-11-036-317-940292	Sequence 940292, A
38	14.2	71.0	25	10	US-11-036-317-975516	Sequence 975516, A
39	14	70.0	20	3	US-09-758-881-19	Sequence 881-19, Appl
40	14	70.0	20	9	US-10-773-678-19	Sequence 19, Appl
41	14	70.0	25	7	US-10-719-956-410880	Sequence 410880, A
42	14	70.0	25	8	US-10-719-900-718599	Sequence 718599, A
43	14	70.0	25	10	US-11-036-317-649659	Sequence 649659, A
44	13.8	69.0	21	8	US-10-751-736-54781	Sequence 54781, A
45	13.8	69.0	21	8	US-10-751-736-54784	Sequence 54784, A

ALIGNMENTS

RESULT 1
US-10-773-678-342
; Sequence 342, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10773.678
; PRIOR FILING DATE: 2004-02-06
; PRIOR FILING DATE: 10/713.139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 342
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-342
Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GACTCTTGACGAGCGGCT 20
Db 1 GACTCTTGACGAGCGGCT 20
RESULT 2
US-10-773-678-158/c
; Sequence 158, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3

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; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-773-678-158

Query Match          100.0%; Score 20; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GACTCTTGCAGGAAGCGGCT 20
Db      26 GACTCTTGCAGGAAGCGGCT 7

RESULT 3
US-10-773-678-179
; Sequence 179, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-179

Query Match          95.0%; Score 19; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GACTCTTGCAGGAAGCGGC 19
Db      2 GACTCTTGCAGGAAGCGGC 20

RESULT 4
US-10-773-678-341
; Sequence 341, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 343
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-343

Query Match          90.0%; Score 18; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GACTCTTGCAGGAAGCGG 18
Db      3 GACTCTTGCAGGAAGCGG 20

RESULT 6
US-10-773-678-340
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; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 341
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-341

Query Match          95.0%; Score 19; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ACTCTTGCAGGAAGCGGCT 20
Db      1 ACTCTTGCAGGAAGCGGCT 19

RESULT 5
US-10-773-678-343
; Sequence 343, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 343
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-343

Query Match          90.0%; Score 18; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GACTCTTGCAGGAAGCGG 18
Db      3 GACTCTTGCAGGAAGCGG 20

RESULT 6
US-10-773-678-340
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; Sequence 340, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 340
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-340

Query Match 85.0%; Score 17; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGCGGCT 20
|||||
Db 1 TCTTGCAGGAGCGGCT 17

RESULT 7
US-10-773-678-344
; Sequence 344, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 344
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-344

Query Match 85.0%; Score 17; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGCG 17
|||||
Db 4 GACTCTTCAGGAGCG 20

RESULT 8
US-10-956-157-186717/c
; Sequence 186717, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 186717
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-186717

Query Match 82.0%; Score 16.4; DB 9; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGCGG 18
|||||
Db 20 GACTCTTCAGGAGCGG 3

RESULT 9
US-10-857-715-201
; Sequence 201, Application US/10857715
; Publication No. US20050164218A1
; GENERAL INFORMATION:
; APPLICANT: Agus David
; APPLICANT: Baker Joffre
; APPLICANT: Natale Ron
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Gene Expression Markers for Response to
; FILE REFERENCE: 39740/0011
; CURRENT APPLICATION NUMBER: US/10/857,715
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/474,908
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: reverse primer
US-10-857-715-201

Query Match 80.0%; Score 16; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CTTGCAGGAGCGGCT 20
|||||
Db 1 CTTGCAGGAGCGGCT 16

RESULT 10
US-10-956-157-301412/c
; Sequence 301412, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

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; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 301412
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
; US-10-956-157-301412

Query Match          76.0%; Score 15.2; DB 9; Length 25;
Best Local Similarity 85.0%; Pred. No. 8.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAGCGGCT 20
Db 23 GCCTTTCGACGAAGCGGCT 4

RESULT 11
US-11-060-756-287536/c
; Sequence 287536, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drg
; FILE REFERENCE: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 287536
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe
; US-11-060-756-287536

Query Match          76.0%; Score 15.2; DB 10; Length 25;
Best Local Similarity 85.0%; Pred. No. 8.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAGCGGCT 20
Db 23 GCCTTTCGACGAAGCGGCT 4

RESULT 12
US-10-773-678-339
; Sequence 339, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karraas, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 339
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-135575
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-339

Query Match          75.0%; Score 15; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TTGCAGGAAGCGGCT 20
Db 1 TTGCAGGAAGCGGCT 15

RESULT 13
US-10-773-678-345
; Sequence 345, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karraas, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 345
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-345

Query Match          75.0%; Score 15; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAG 15
Db 6 GACTCTTGCAGGAAG 20

RESULT 14
US-10-719-956-135575/c
; Sequence 135575, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 135575
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-135575
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RESULT 17
US-10-809-189-124305/c
; Sequence 124305, Application US/10809189
; Publication No. US2005004831A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mitmann

```

```

, GENERAL INFORMATION.
, APPLICANT: xue Mei Zhou
, TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
, FILE REFERENCE: 3528.1
, CURRENT APPLICATION NUMBER: US/10/719,900
, CURRENT FILING DATE: 2003-11-20
, PRIOR APPLICATION NUMBER: 60/427,808
, PRIOR FILING DATE: 2002 11 20
, NUMBER OF SEQ ID NOS: 982914
, SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
, SEQ ID NO 611442
, LENGTH: 25
,

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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-611442

Query Match      72.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CTTGCAGGAGCGGCT 20
   ||||| ||||| |||||
Db 19 CTTGCAGGAGCAGCT 4

RESULT 20
US-10-956-157-178444/c
; Sequence 178444, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178444
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-178444

Query Match      72.0%; Score 14.4; DB 9; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CTTGCAGGAGCGGCT 20
   ||||| ||||| |||||
Db 21 CTTCCAGGAGCGGCT 6

RESULT 21
US-11-036-317-95537/c
; Sequence 95537, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 95537
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-95537

Query Match      72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTTGACGAGGAGCGGC 19
   ||||| ||||| |||||
Db 20 TCGTGACGAGGAGCGGC 5

RESULT 22
US-10-773-678a-342.max30.rnpbm

US-10-751-736-54782/c
; Sequence 54782, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751.736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54782
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai
US-10-751-736-54782

Query Match      71.0%; Score 14.2; DB 8; Length 21;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTGACGAGGAGCGGCT 20
   ||||| ||||| |||||
Db 21 AATCTTCTAGGAGCGGCT 3

RESULT 23
US-10-719-956-51664/c
; Sequence 51664, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719.956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 51664
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-51664

Query Match      71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTGACGAGGAGCGGCT 20
   ||||| ||||| |||||
Db 20 ACTCTTACAGGAGCGGCT 2

RESULT 24
US-10-809-189-65325
; Sequence 65325, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
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; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65325
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-65325

Query Match 71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGGAGCGGCT 20
Db 5 ACTCTTCAGGAGGCT 23

RESULT 25

US-11-036-317-193968
; Sequence 193968, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 193968
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-193968

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGCGGC 19
Db 5 GACCCCTGCAGGAGTGCC 23

RESULT 26

US-11-036-317-247028
; Sequence 247028, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 247028
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-247028

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGCGGC 19
Db 3 GACCCCTGCAGGAGTGCC 21

RESULT 27

US-11-036-317-255809
; Sequence 255809, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 255809
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-255809

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGCGGC 19
Db 2 GACCCCTGCAGGAGTGCC 20

RESULT 28

US-11-036-317-289853
; Sequence 289853, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 289853
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-289853

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGCGGC 19
Db 1 GACCCCTGCAGGAGTGCC 19

RESULT 29

US-11-036-317-308860
; Sequence 308860, Application US/11036317
; Publication No. US20050214823A1


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RESULT 34
US-11-036-317-634153/c
; Sequence 634153, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 634153
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-634153

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTGCGAGGAGCGGCT 20
Db 21 ATTCTGCGAGGAGCGGCT 3

RESULT 35
US-11-036-317-648448
; Sequence 648448, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 648448
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-648448

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTGCGAGGAGCGGCT 20
Db 21 ATTCTGCGAGGAGCGGCT 3

RESULT 36
US-11-036-317-773627
; Sequence 773627, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
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; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 773627
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-773627

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGCGAGGAGCGGC 19
Db 6 GACTCTTGCGAGGAGCGGC 24

RESULT 37
US-11-036-317-940292
; Sequence 940292, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 940292
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-940292

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTGCGAGGAGCGGCT 20
Db 7 ACTCTTGCGAGGAGCGGCT 25

RESULT 38
US-11-036-317-975516
; Sequence 975516, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036.317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 975516
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-975516

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGCGAGGAGCGGC 19
```

Db 2 GACTACTGCAGCGCGC 20
||||| ||||| ||||| |||||

RESULT 39
US-09-758-881-19
; Sequence 19, Application US/09758881
; Patent No. US20010029250A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0532
; CURRENT FILING DATE: 2001-01-11
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-881-19

Query Match 70.0%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAA 14
Db 7 GACTCTTGCAGGAA 20
||||| ||||| ||||| |||||

RESULT 40
US-10-773-678-19
; Sequence 19, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR FILING DATE: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-773-678-19

Query Match 70.0%; Score 14; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAA 14
||||| ||||| ||||| |||||

Db 7 GACTCTTGCAGGAA 20

Search completed: December 3, 2005, 15:23:05
Job time : 796 secs

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November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published Applications New databases; older published applications make up the Published Applications Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions **rnbpn** (Published Applications NA_Main) and **rnbpn** (Published Applications NA_New).

Searches run against Amino Acid Published Applications produce two sets of results, with the extensions **rapbn** (Published Applications AA_Main) and **rapbn** (Published Applications AA_New).

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:30:06 ; Search time 233 Seconds
(without alignments)
26.714 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactctgcaggagcgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6442102

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

- 1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
(score greater than or equal to the score of the result being printed,
And is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	80.0	20	7	US-11-102-228-233
2	14.4	72.0	19	8	US-11-101-244-1290351
3	14.4	72.0	19	9	US-11-083-784-1290351
4	13.8	69.0	19	8	US-11-101-244-439270
5	13.8	69.0	19	9	US-11-083-784-439270
6	13.4	67.0	19	8	US-11-101-244-1290317
7	13.4	67.0	19	9	US-11-083-784-1290317
8	13.2	66.0	19	8	US-11-101-244-556327
9	13.2	66.0	19	9	US-11-083-784-556327
10	13	65.0	19	8	US-11-101-244-968731
11	13	65.0	19	9	US-11-101-244-968731
12	13	65.0	19	8	US-11-101-244-968803
13	13	65.0	19	9	US-11-083-784-968731
14	13	65.0	19	9	US-11-083-784-968803
15	13	65.0	19	8	US-11-083-784-1066415
16	12.8	64.0	19	8	US-11-101-244-21319
17	12.8	64.0	19	9	US-11-101-244-1169015
18	12.8	64.0	19	8	US-11-101-244-1552463
19	12.8	64.0	19	9	US-11-101-244-1585494
20	12.8	64.0	19	8	US-11-083-784-21319
21	12.8	64.0	19	9	US-11-083-784-1169015
22	12.8	64.0	19	9	US-11-083-784-1552463
23	12.8	64.0	19	9	US-11-083-784-1585494

24	12.8	64.0	22	6	US-10-750-185-14564	Sequence 14564, A
c 25	12.6	63.0	20	7	US-11-090-739-13	Sequence 13, Appl
c 26	12.4	62.0	19	8	US-11-101-244-251435	Sequence 251435, A
c 27	12.4	62.0	19	8	US-11-101-244-251481	Sequence 251481, A
c 28	12.4	62.0	19	8	US-11-101-244-1337482	Sequence 1337482, A
c 29	12.4	62.0	19	9	US-11-083-784-251435	Sequence 251435, A
c 30	12.4	62.0	19	9	US-11-083-784-251481	Sequence 251481, A
c 31	12.4	62.0	19	9	US-11-083-784-1337482	Sequence 1337482, A
c 32	12.2	61.0	19	8	US-11-101-244-186562	Sequence 186562, A
c 33	12.2	61.0	19	8	US-11-101-244-199830	Sequence 199830, A
c 34	12.2	61.0	19	8	US-11-101-244-266845	Sequence 266845, A
c 35	12.2	61.0	19	8	US-11-101-244-266905	Sequence 266905, A
c 36	12.2	61.0	19	8	US-11-101-244-277581	Sequence 277581, A
c 37	12.2	61.0	19	8	US-11-101-244-487058	Sequence 487058, A
c 38	12.2	61.0	19	8	US-11-101-244-726311	Sequence 726311, A
c 39	12.2	61.0	19	8	US-11-101-244-855529	Sequence 855529, A
c 40	12.2	61.0	19	8	US-11-101-244-1268245	Sequence 1268245, A
c 41	12.2	61.0	19	8	US-11-101-244-1268345	Sequence 1268345, A
c 42	12.2	61.0	19	8	US-11-101-244-1270630	Sequence 1270630, A
c 43	12.2	61.0	19	8	US-11-101-244-1455586	Sequence 1455586, A
c 44	12.2	61.0	19	8	US-11-101-244-1511826	Sequence 1511826, A
c 45	12.2	61.0	19	8	US-11-101-244-1531334	Sequence 1531334, A

ALIGNMENTS

RESULT 1
US-11-102-228-233
; Sequence 233, Application US/11102228
; Publication No. US20050260646A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, JOFFRE B.
; APPLICANT: SHAK, STEVEN
; APPLICANT: GIANNI, LUCA
; TITLE OF INVENTION: GENE EXPRESSION MARKERS FOR PREDICTING
; TITLE OF INVENTION: RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: 39740-0017
; CURRENT APPLICATION NUMBER: US/11/102.228
; CURRENT FILING DATE: 2005-04-07
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Reverse Primer
US-11-102-228-233

Query Match 80.0%; Score 16; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CTTGAGGAGCGGCT 20
|||||
Db 1 CTTGAGGAGCGGCT 16

RESULT 2
US-11-101-244-1290351/c
; Sequence 1290351, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244

; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1290351
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1290351

Query Match 72.0%; Score 14.4; DB 8; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGC 19
|||||
Db 16 TCTTGCAGGAAGCAGC 1

RESULT 3

US-11-083-784-1290351/c
; Sequence 1290351, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1290351
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1290351

Query Match 72.0%; Score 14.4; DB 9; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGC 19
|||||
Db 16 TCTTGCAGGAAGCAGC 1

RESULT 4

US-11-101-244-439270/c
; Sequence 439270, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 439270
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-439270

Query Match 69.0%; Score 13.8; DB 8; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACTCTTGACGGAAGCGG 18
|||||
Db 17 ACTCTTGAGGGAAGCGG 1

RESULT 5

US-11-083-784-439270/c
; Sequence 439270, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 439270
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-439270

Query Match 69.0%; Score 13.8; DB 9; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACTCTTGACGGAAGCGG 18
|||||
Db 17 ACTCTTGAGGGAAGCGG 1

RESULT 6

US-11-101-244-1290317/c
; Sequence 1290317, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

```

; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1290317
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1290317

```

```

Query Match 67.0%; Score 13.4; DB 8; Length 19;
Best Local Similarity 93.3%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TTGCAGGAAGCGGCT 20
    ||||| ||||| |||
Db 19 TTGCAGGAAGCAGCT 5

```

```

RESULT 7
US-11-083-784-1290317/c
; Sequence 1290317, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1290317
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1290317

```

```

Query Match 67.0%; Score 13.4; DB 9; Length 19;
Best Local Similarity 93.3%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TTGCAGGAAGCGGCT 20
    ||||| ||||| |||
Db 19 TTGCAGGAAGCAGCT 5

```

```

RESULT 8
US-11-101-244-556327/c
; Sequence 556327, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 556327
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-556327

```

```

Query Match 66.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 83.3%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGGAAGCGGC 19
    ||||| ||||| |||
Db 18 ACTCTTCAGGAGCTGC 1

```

```

RESULT 9
US-11-083-784-556327/c
; Sequence 556327, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 556327
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-556327

```

```

Query Match 66.0%; Score 13.2; DB 9; Length 19;
Best Local Similarity 83.3%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGGAAGCGGC 19
    ||||| ||||| |||
Db 18 ACTCTTCAGGAGCTGC 1

```

```

RESULT 10
US-11-101-244-968731
; Sequence 968731, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 968731
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-968731

Query Match 65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 6.7e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGACGAAGC 16
Db 3 UCUGCAGGAAGC 15

RESULT 11
US-11-101-244-968803
; Sequence 968803, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 968803
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-968803

Query Match 65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 6.7e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGACGAAGC 16
Db 3 UCUGCAGGAAGC 15

RESULT 12
US-11-101-244-1066415
; Sequence 1066415, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1066415
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1066415

Query Match 65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 92.3%; Pred. No. 6.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GCAGGAAGCGGCT 20
Db 1 GCAGGAAGCGGCU 13

RESULT 13
US-11-083-784-968731
; Sequence 968731, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 968731
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-968731

Query Match 65.0%; Score 13; DB 9; Length 19;
Best Local Similarity 76.9%; Pred. No. 6.7e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGACGAAGC 16
Db 3 UCUGCAGGAAGC 15

RESULT 14
US-11-083-784-968803
; Sequence 968803, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 968803
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-968803

Query Match 65.0%; Score 13; DB 9; Length 19;
Best Local Similarity 76.9%; Pred. No. 6.7e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGC 16
Db 3 UCUUGCAGGAGC 15

RESULT 15
US-11-083-784-1066415
Sequence 1066415, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmakon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1066415
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-1066415

Query Match 65.0%; Score 13; DB 9; Length 19;
Best Local Similarity 92.3%; Pred. No. 6.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GCAGGAGCGGCT 20
Db 1 GCAGGAGCGGCU 13

RESULT 16
US-11-101-244-21319/c
Sequence 21319, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmakon, Inc.
APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 21319
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-21319

Query Match 64.0%; Score 12.8; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGCGC 19
Db 17 TCTTGAAGGAAGTGGC 2

RESULT 17
US-11-101-244-1169015/c
Sequence 1169015, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmakon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1169015
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1169015

Query Match 64.0%; Score 12.8; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGC 16
Db 19 GAATCTGCGCAGGAGC 4

RESULT 18
US-11-101-244-1552463/c
Sequence 1552463, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmakon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1552463
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1552463

Query Match 64.0%; Score 12.8; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACTCTTGCAGGAGCG 17
||||| ||||| |||||
Db 19 ACTCATGCGAGATGCG 4

RESULT 19

US-11-101-244-1585494/c
; Sequence 1585494, Application US/11/101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1585494
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1585494

Query Match 64.0%; Score 12.8; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGC 16
||| ||| ||||| |||||
Db 19 GAATCTGCGAGGAGC 4

RESULT 20

US-11-083-784-21319/c
; Sequence 21319, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 21319
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-21319

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGCGC 19
||||| ||||| |||||
Db 17 TCTTGAAGGAGGTGC 2

RESULT 21

US-11-083-784-1169015/c
; Sequence 1169015, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1169015
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1169015

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGC 16
||| ||| ||||| |||||
Db 19 GAATCTGCGAGGAGC 4

RESULT 22

US-11-083-784-1552463/c
; Sequence 1552463, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1552463
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1552463

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACTCTTGCAGGAGCG 17
||||| ||||| ||||| |||||
Db 19 ACTCATGCAGGATGCG 4

RESULT 23
US-11-083-784-1585494/c
; Sequence 1585494, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1585494
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1585494

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGCG 16
||| ||| ||||| |||||
Db 19 GAATCTGCAGGAGCG 4

RESULT 24
US-10-750-185-14564
; Sequence 14564, Application US/10750185

; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14564
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-185-14564

Query Match 64.0%; Score 12.8; DB 6; Length 22;
Best Local Similarity 87.5%; Pred. No. 8.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACTCTTGCAGGAGCG 17
||||| ||||| ||||| |||||
Db 7 ACTCTTGCAGGAGCG 22

RESULT 25
US-11-090-739-13/c
; Sequence 13, Application US/11090739
; Publication No. US20050260639A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Yusuke
; APPLICANT: KATAGIRI, Toyomasa
; APPLICANT: NAKAGAWA, Hirowaki
; TITLE OF INVENTION: METHOD FOR DIAGNOSING PANCREATIC CANCER
; FILE REFERENCE: 082368-003600US
; CURRENT APPLICATION NUMBER: US/11/090,739
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: PCT/JP2003/011817
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/555,809
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/450,889
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/414,872
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificially synthesized primer sequence for RT-PCR
US-11-090-739-13

Query Match 63.0%; Score 12.6; DB 7; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGCAGGAGCGGCT 20
||| ||| ||||| |||||
Db 20 AATCTCCAGGAGGCTGCT 2

RESULT 26

US-11-101-244-251435/c
; Sequence 251435, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 251435
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-251435

Query Match 62.0%; Score 12.4; DB 8; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAAG 15
|||||
Db 18 ACTCTTGCAGGTAG 5

RESULT 27

US-11-101-244-251481/c
; Sequence 251481, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 251481
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-251481

Query Match 62.0%; Score 12.4; DB 8; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAAG 15
|||||
Db 17 ACTCTTGCAGGTAG 4

RESULT 28

US-11-101-244-1337482/c
; Sequence 1337482, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1337482
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1337482

Query Match 62.0%; Score 12.4; DB 8; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAAG 15
|||||
Db 18 ACTCTTGCAGGAAG 5

RESULT 29

US-11-083-784-251435/c
; Sequence 251435, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 251435
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-251435

Query Match 62.0%; Score 12.4; DB 9; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAAG 15
|||||
Db 18 ACTCTTGCAGGTAG 5

RESULT 30
US-11-083-784-251481/c
; Sequence 251481, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 251481
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-251481

Query Match 62.0%; Score 12.4; DB 9; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAAG 15
|||||

Db 17 ACTCTTGCAGGTAG 4

RESULT 31
US-11-083-784-1337482/c
; Sequence 1337482, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1337482
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1337482

Query Match 62.0%; Score 12.4; DB 9; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAAG 15
|||||

Db 18 ACTCTTGCAGGAAG 5

RESULT 32
US-11-101-244-186562/c
; Sequence 186562, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 186562
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-186562

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAAGCGCT 20
|||||

Db 19 TCTTGCAGGAACCGGT 3

RESULT 33
US-11-101-244-199830/c
; Sequence 199830, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 199830
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-199830

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAAGCGCT 20
|||||

Db 19 TCATGCAGCAAGTGGCT 3

RESULT 34

US-11-101-244-266845/c
; Sequence 266845, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 266845
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-266845

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCTTCGAGGAGCGGC 19
||| ||||| |||||
Db 17 CTCTTCGAGGTAGCGGC 1

RESULT 35

US-11-101-244-266905/c
; Sequence 266905, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 266905
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-266905

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCTTCGAGGAGCGGC 19
||| ||||| |||||
Db 17 CTCTTCGAGGTAGCGGC 1

RESULT 36

US-11-101-244-277581/c
; Sequence 277581, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 277581
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-277581

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCTTCGAGGAAGCGGCT 20
||| ||||| |||||
Db 19 TCATTCAGATCGGCT 3

RESULT 37

US-11-101-244-487058/c
; Sequence 487058, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 487058
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-487058

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCTTCGAGGAAGCGGCT 20
||| ||||| |||||
Db 19 TCATTCAGGAAGCGGCT 3

RESULT 38

US-11-101-244-726311/c
; Sequence 726311, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726311
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-726311

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCTTCAGGAGCGGCT 20
| | | | | | | | | |
Db 19 TCTTCAGGAGCGGCT 3

RESULT 39

US-11-101-244-855529/c
; Sequence 855529, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 855529
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-855529

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCTTCAGGAGCGGCT 20
| | | | | | | | | |
Db 18 TGTTCAGGAGAGGCT 2

RESULT 40

US-11-101-244-1268245/c
; Sequence 1268245, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1268245
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1268245

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCTTCAGGAGCGGC 19
| | | | | | | | | |
Db 17 CTGTTTCAGGAGCTGC 1

Search completed: December 3, 2005, 15:27:10
Job time : 234 secs

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